<110> Lu, Peter S.
     Carman, Jonathan D.
     Candia III, Albert F.
     Arbbor Vita Corporation

<120> CLASP-2 TRANSMEMBRANE PROTEINS

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gag ttg ccc act cag ctg cat gaa aag cac cac ctg ttg ctc aca ttc    97
Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe
             20                  25                  30

ttc cat gtc agc tgt gac aac tca agt aaa gga agc acg aag aag agg   145
Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg
             35                  40                  45

gat gtc gtt gaa acc caa gtt ggc tac tcc tgg ctt ccc ctc ctg aaa   193
Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys
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gac gga agg gtg gtg aca agc gag cag cac atc ccg gtc tcg gcg aac   241
Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn
 65                  70                  75                  80

ctt cct tcg ggc tat ctt ggc tac caa gag ctt ggg atg ggc agg cat   289
Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His
                 85                  90                  95

tat ggt ccg gaa att aaa tgg gta gat gga ggc aag cca ctg ctg aaa   337
Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys
                100                 105                 110

att tcc act cat ctg gtt tct aca gtg tat act cag gat cag cat tta   385
Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu
             115                 120                 125

cat aat ttt ttc cag tac tgt cag aaa acc gaa tct gga gcc caa gcc   433
His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala
     130                 135                 140

tta gga aac gaa ctt gta aag tac ctt aag agt ctg cat gcg atg gaa   481
Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu
145                 150                 155                 160

ggc cac gtg atg atc gcc ttc ttg ccc act atc cta aac cag ctg ttc   529
Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe
                165                 170                 175

cga gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt aac gtg act   577
Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr
             180                 185                 190

cgg gtc att att cat gtg gtt gcc cag tgc cat gag gaa gga ttg gag   625
Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu
         195                 200                 205

agc cac ttg agg tca tat gtt aag tac gcg tat aag gct gag cca tat   673
Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr
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gtt gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc aaa tcc atg   721
Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met
225                 230                 235                 240
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2

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Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu
            245             250             255

ctg agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa tct atg gct    817
Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala
            260             265             270

cag cat ttg ata gag aac tcc aaa gtt aag ttg ctg cga aac cag aga    865
Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg
            275             280             285

ttt cct gca tcc tat cat cat gca gcg gaa acc gtt gta aat atg ctg    913
Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu
            290             295             300

atg cca cac atc act cag aag ttt gga gat aat cca gag gca tct aag    961
Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys
305             310             315             320

aac gcg aat cat agc ctt gct gtc ttc atc aag aga tgt ttc acc ttc   1009
Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe Thr Phe
                325             330             335

atg gac agg ggc ttt gtc ttc aag cag atc aac aac tac att agc tgt   1057
Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys
            340             345             350

ttt gct cct gga gac cca aag acc ctc ttt gaa tac aag ttt gaa ttt   1105
Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe
            355             360             365

ctc cgt gta gtg tgc aac cat gaa cat tat att ccg ttg aac tta cca   1153
Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro
            370             375             380

atg cca ttt gga aaa ggc agg att caa aga tac caa gac ctc cag ctt   1201
Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu
385             390             395             400

gac tac tca tta aca gat gag ttc tgc aga aac cac ttc ttg gtg gga   1249
Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly
                405             410             415

ctg tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc cgg gag gtc   1297
Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg Glu Val
            420             425             430

cgt ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata aag cat tct   1345
Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser
            435             440             445

ttt gat gac aga tat gct tca agg agc cat cag gca agg ata gcc acc   1393
Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile Ala Thr
            450             455             460

ctc tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc cag cgg atc   1441
Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln Arg Ile
465             470             475             480

aat gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc atg acc gtg   1489
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3

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Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met Thr Val
                485             490                 495

aag gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg gtg acg ccg     1537
Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val Thr Pro
            500             505                 510

cag aag gga agc acc ctg gac aac agc ctg cac aag gac ctg ctg ggc     1585
Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu Leu Gly
            515             520                 525

gcc atc tcc ggc att gct tct cca tat aca acc tca act cca aac atc     1633
Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile
    530             535                 540

aac agt gtg aga aat gct gat tcg aga gga tct ctc ata agc aca gat     1681
Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp
545             550                 555                 560

tcg ggt aac agc ctt cca gaa agg aat agt gag aag agc aat tcc ctg     1729
Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu
                565             570                 575

gat aag cac caa caa agt agc aca ttg gga aat tcc gtg gtt cgc tgt     1777
Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys
            580             585                 590

gat aaa ctt gac cag tct gag att aag agc cta ctg atg tgt ttc ctc     1825
Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu
            595             600                 605

tac atc tta aag agc atg tct gat gat gct ttg ttt aca tat tgg aac     1873
Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn
    610             615                 620

aag gct tca aca tct gaa ctt atg gat ttt ttt aca ata tct gaa gtc     1921
Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val
625             630                 635                 640

tgc ctg cac cag ttc cag tac atg ggg aag cga tac ata gcc agg aac     1969
Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn
                645             650                 655

cag gag ggg ttg gga ccc ata gtt cat gat cga aag tct cag aca ttg     2017
Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu
            660             665                 670

cct gtt tcc cgt aac aga aca gga atg atg cat gcc aga ttg cag cag     2065
Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln
            675             680                 685

ctg ggc agc ctg gat aac tct ctc act ttt aac cac agc tat ggc cac     2113
Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His
            690             695                 700

tcg gac gca gat gtt ctg cac cag tca tta ctt gaa gcc aac att gct     2161
Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala
705             710                 715                 720

act gag gtt tgc ctg aca gct ctg gac acg ctt tct cta ttt aca ttg     2209
Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu
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4

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gcg ttt aag aac cag ctc ctg gcc gac cat gga cat aat cct ctc atg   2257
Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met
            740                 745                 750

aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag tct   2305
Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser
            755                 760                 765

gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc tta att tat   2353
Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr
        770                 775                 780

aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg gct   2401
Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala
785             790                 795                 800

ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc atc   2449
Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile
                805                 810                 815

agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac ttt   2497
Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe
            820                 825                 830

gat tac act gga aag aag tcc ttt gtc cgg aca cat ttg caa gtc atc   2545
Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile
        835                 840                 845

ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gaa acc   2593
Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr
        850                 855                 860

aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt gac   2641
Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp
865             870                 875                 880

cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag gac tta acc   2689
Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr
                885                 890                 895

aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg aag gag cat   2737
Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His
            900                 905                 910

gag aac gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc aaa   2785
Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys
        915                 920                 925

tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc atg   2833
Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met
        930                 935                 940

gcc agg atc cat gtc aaa aat ggc gat ctc tca gag gca gca atg tgc   2881
Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys
945             950                 955                 960

tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa ggc   2929
Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly
                965                 970                 975
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5

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gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc cca aac atc    2977
Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile
            980                 985                 990

gac gag gag gcc tcc atg atg gaa gac gtg ggg atg cag gat gtc cat    3025
Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His
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ttc aac gag gat gtg ctg atg gag ctc ctt gag cag tgc gca gat gga    3073
Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly
            1010                1015                1020

ctc tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc tac aaa ctt    3121
Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu
1025                1030                1035                1040

atc atc ccc att tat gag aag cgg agg gat ttc ttt gaa gat gaa gat    3169
Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp
                    1045                1050                1055

gga aag gag tat att tac aag gaa ccc aaa ctc aca ccg ctg tcg gaa    3217
Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu
            1060                1065                1070

att tct cag aga ctc ctt aaa ctg tac tcg gat aaa ttt ggt tct gaa    3265
Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu
            1075                1080                1085

aat gtc aaa atg ata cag gat tct ggc aag gtc aac cct aag gat ctg    3313
Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu
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gat tct aag tat gca tac atc cag gtg act cac gtc atc ccc ttc ttt    3361
Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe
1105                1110                1115                1120

gac gaa aaa gag ttg caa gaa agg aaa aca gag ttt gag aga tcc cac    3409
Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His
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aac atc cgc cgc ttc atg ttt gag atg cca ttt acg cag acc ggg aag    3457
Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys
            1140                1145                1150

agg cag ggc ggg gtg gaa gag cag tgc aaa cgg cgc acc atc ctg aca    3505
Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
            1155                1160                1165

gcc ata cac tgc ttc cct tat gtg aag aag cgc atc cct gtc atg tac    3553
Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr
1170                1175                1180

cag cac cac act gac ctg aac ccc atc gag gtg gcc att gac gag atg    3601
Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met
1185                1190                1195                1200

agt aag aag gtg gcg gag ctc cgg cag ctg tgc tcc tcg gcc gag gtg    3649
Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val
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6

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gac atg atc aaa ctg cag ctc aaa ctc cag ggc agc gtg agt gtt cag        3697
Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln
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gtc aat gct ggc cca cta gca tat gcg cga gct ttc tta gat gat aca        3745
Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
         1235             1240                 1245

aac aca aag cga tat cct gac aat aaa gtg aag ctg ctt aag gaa gtt        3793
Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
         1250             1255                 1260

ttc agg caa ttt gtg gaa gct tgc ggt caa gcc tta gcg gta aac gaa        3841
Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
1265             1270                 1275                 1280

cgt ctg att aaa gaa gac cag ctc gag tat cag gaa gaa atg aaa gcc        3889
Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
             1285                 1290                 1295

aac tac agg gaa atg gcg aag gag ctt tct gaa atc atg cat gag cag        3937
Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
         1300             1305                 1310

atc tgc ccc ctg gag gag aag acg agc gtc tta ccg aat tcc ctt cac        3985
Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
         1315             1320                 1325

atc ttc aac gcc atc agt ggg act cca aca agc aca atg gtt cac ggg        4033
Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
         1330             1335                 1340

atg acc agc tcg tct tcg gtc gtg tga ttacatctca tggcccgtgt             4080
Met Thr Ser Ser Ser Ser Val Val
1345             1350

gtggggactt gctttgtcat ttgcaaactc aggatgcttt ccaaagccaa tcactgggga     4140

gaccgagcac agggaggacc aaggggaagg ggagagaaag gaaataaaga caacgttat      4200

ttcttaacag actttctata ggagttgtaa gaaggtgcac atattttttt aaatctcact     4260

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gcctcgactc gtgccggaaa tctgatcgta atcagggtac agaacttact agttttgtct     4500

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ctcacatggg cttatgcatt aagtttaatt gtgataaatt tgtgctggtc cagtatatgc     4740

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(CLASP-2A)

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Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg
        35                  40                  45
Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys
    50                  55                  60
Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn
65                  70                  75                  80
Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His
                85                  90                  95
Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys
            100                 105                 110
Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu
        115                 120                 125
His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala
    130                 135                 140
Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu
145                 150                 155                 160
Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe
                165                 170                 175
Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr
            180                 185                 190
Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu
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Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr
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Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met
225                 230                 235                 240
Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu
            245                 250                 255
Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala
        260                 265                 270
Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg
    275                 280                 285
Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu
    290                 295                 300
Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys
305                 310                 315                 320
Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe Thr Phe
                325                 330                 335
Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys
            340                 345                 350
Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe
        355                 360                 365
Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro
    370                 375                 380
Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu
385                 390                 395                 400
Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly
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8

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                    405                      410                      415
Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg Glu Val
            420                  425                  430
Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser
        435                  440                  445
Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile Ala Thr
    450                  455                  460
Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln Arg Ile
465                  470                  475                  480
Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met Thr Val
                485                  490                  495
Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val Thr Pro
            500                  505                  510
Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu Leu Gly
        515                  520                  525
Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile
    530                  535                  540
Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp
545                  550                  555                  560
Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu
                565                  570                  575
Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys
            580                  585                  590
Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu
        595                  600                  605
Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn
    610                  615                  620
Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val
625                  630                  635                  640
Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn
                645                  650                  655
Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu
            660                  665                  670
Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln
        675                  680                  685
Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His
        690                  695                  700
Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala
705                  710                  715                  720
Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu
                725                  730                  735
Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met
            740                  745                  750
Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser
        755                  760                  765
Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr
    770                  775                  780
Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala
785                  790                  795                  800
Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile
                805                  810                  815
Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe
            820                  825                  830
Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile
        835                  840                  845
Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr
    850                  855                  860
Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp
865                  870                  875                  880
Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr
            885                  890                  895
```

9

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Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His
            900                     905                 910
Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys
            915                     920                 925
Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met
            930                     935                 940
Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys
945                     950                 955                 960
Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly
                965                     970                 975
Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile
            980                     985                 990
Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His
            995                     1000                1005
Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly
    1010                    1015                1020
Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu
1025                    1030                1035                1040
Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp
                1045                    1050                1055
Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu
            1060                    1065                1070
Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu
    1075                    1080                1085
Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu
    1090                    1095                1100
Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe
1105                    1110                1115                1120
Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His
            1125                    1130                1135
Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys
            1140                    1145                1150
Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr
        1155                    1160                1165
Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr
    1170                    1175                1180
Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met
1185                    1190                1195                1200
Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val
            1205                    1210                1215
Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln
            1220                    1225                1230
Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr
    1235                    1240                1245
Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val
    1250                    1255                1260
Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu
1265                    1270                1275                1280
Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala
            1285                    1290                1295
Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln
            1300                    1305                1310
Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His
    1315                    1320                1325
Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly
    1330                    1335                1340
Met Thr Ser Ser Ser Ser Val Val
1345                    1350
```

10

<210> 3
<211> 3705
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(3702)

<220>
<223> Human cadherin-like asymmetry protein 2B
      (CLASP-2B)

<400> 3
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gcg atg gaa ggc cac gtg atg atc gcc ttc ttg ccc act atc cta aac      48
Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn
 1               5                  10                  15

cag ctg ttc cga gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt      96
Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val
                20                  25                  30

aac gtg act cgg gtc att att cat gtg gtt gcc cag tgc cat gag gaa     144
Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu
            35                  40                  45

gga ttg gag agc cac ttg agg tca tat gtt aag tac gcg tat aag gct     192
Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala
        50                  55                  60

gag cca tat gtt gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc     240
Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
65                  70                  75                  80

aaa tcc atg acc acg att ctc aag cct tct gcc gat ttc ctc acc agc     288
Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
                85                  90                  95

aac aaa cta ctg agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa     336
Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys
               100                 105                 110

tct atg gct cag cat ttg ata gag aac tcc aaa gtt aag ttg ctg cga     384
Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg
           115                 120                 125

aac cag aga ttt cct gca tcc tat cat cat gca gcg gaa acc gtt gta     432
Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val
       130                 135                 140

aat atg ctg atg cca cac atc act cag aag ttt gga gat aat cca gag     480
Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu
145                 150                 155                 160

gca tct aag aac gcg aat cat agc ctt gct gtc ttc atc aag aga tgt     528
Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys
                165                 170                 175

ttc acc ttc atg gac agg ggc ttt gtc ttc aag cag atc aac aac tac     576
Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr
               180                 185                 190
```

11

```
att agc tgt ttt gct cct gga gac cca aag acc ctc ttt gaa tac aag    624
Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
        195             200             205

ttt gaa ttt ctc cgt gta gtg tgc aac cat gaa cat tat att ccg ttg    672
Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu
        210             215             220

aac tta cca atg cca ttt gga aaa ggc agg att caa aga tac caa gac    720
Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp
225             230             235             240

ctc cag ctt gac tac tca tta aca gat gag ttc tgc aga aac cac ttc    768
Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
                245             250             255

ttg gtg gga ctg tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc    816
Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
            260             265             270

cgg gag gtc cgt ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata    864
Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
            275             280             285

aag cat tct ttt gat gac aga tat gct tca agg agc cat cag gca agg    912
Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
        290             295             300

ata gcc acc ctc tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc    960
Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
305             310             315             320

cag cgg atc aat gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc   1008
Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
                325             330             335

atg acc gtg aag gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg   1056
Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
            340             345             350

gtg acg ccg cag aag gga agc acc ctg gac aac agc ctg cac aag gac   1104
Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp
        355             360             365

ctg ctg ggc gcc atc tcc ggc att gct tct cca tat aca acc tca act   1152
Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr
        370             375             380

cca aac atc aac agt gtg aga aat gct gat tcg aga gga tct ctc ata   1200
Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile
385             390             395             400

agc aca gat tcg ggt aac agc ctt cca gaa agg aat agt gag aag agc   1248
Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser
            405             410             415

aat tcc ctg gat aag cac caa caa agt agc aca ttg gga aat tcc gtg   1296
Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val
        420             425             430
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12

```
gtt cgc tgt gat aaa ctt gac cag tct gag att aag agc cta ctg atg     1344
Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met
        435             440                 445

tgt ttc ctc tac atc tta aag agc atg tct gat gat gct ttg ttt aca     1392
Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr
        450             455                 460

tat tgg aac aag gct tca aca tct gaa ctt atg gat ttt ttt aca ata     1440
Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile
465             470                 475                 480

tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga tac ata     1488
Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
                485                 490                 495

gcc agg aac cag gag ggg ttg gga ccc ata gtt cat gat cga aag tct     1536
Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser
                500                 505                 510

cag aca ttg cct gtt tcc cgt aac aga aca gga atg atg cat gcc aga     1584
Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg
            515                 520                 525

ttg cag cag ctg ggc agc ctg gat aac tct ctc act ttt aac cac agc     1632
Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser
        530                 535                 540

tat ggc cac tcg gac gca gat gtt ctg cac cag tca tta ctt gaa gcc     1680
Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala
545                 550                 555                 560

aac att gct act gag gtt tgc ctg aca gct ctg gac acg ctt tct cta     1728
Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu
                565                 570                 575

ttt aca ttg gcg ttt aag ctc ctg gcc gac cat gga cat aat cct ctc     1776
Phe Thr Leu Ala Phe Lys Leu Leu Ala Asp His Gly His Asn Pro Leu
            580                 585                 590

atg aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag     1824
Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln
            595                 600                 605

tct gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc tta att     1872
Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile
        610                 615                 620

tat aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg     1920
Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala
625                 630                 635                 640

gct ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc     1968
Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser
                645                 650                 655

atc agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac     2016
Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn
                660                 665                 670

ttt gat tac act gga aag aag tcc ttt gtc cgg aca cat ttg caa gtc     2064
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13

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Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val
        675             680                 685

atc ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gaa    2112
Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu
        690             695                 700

acc aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt    2160
Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser
705             710                 715                 720

gac cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag gac tta    2208
Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu
                725                 730                 735

acc aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg aag gag    2256
Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu
                740             745                 750

cat gag aac gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc    2304
His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala
            755             760                 765

aaa tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc    2352
Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser
770             775                 780

atg gcc agg atc cat gtc aaa aat ggc gat ctc tca gag gca gca atg    2400
Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met
785             790                 795                 800

tgc tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa    2448
Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys
                805                 810                 815

ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc cca aac    2496
Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn
                820             825                 830

atc gac gag gag gcc tcc atg atg gaa gac gtg ggg atg cag gat gtc    2544
Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val
            835             840                 845

cat ttc aac gag gat gtg ctg atg gag ctc ctt gag cag tgc gca gat    2592
His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp
850             855                 860

gga ctc tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc tac aaa    2640
Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys
865             870                 875                 880

ctt atc atc ccc att tat gag aag cgg agg gat ttt gag agg ctg gcc    2688
Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala
                885                 890                 895

cat ctg tat gac acg ctg cac cgg gcc tac agc aaa gtg acc gag gtc    2736
His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val
            900                 905                 910

atg cac tcg ggc cgc agg ctt ctg ggg acc tac ttc cgg gta gcc ttc    2784
Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe
```

14

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ttc ggg cag gga ttc ttt gaa gat gaa gat gga aag gag tat att tac     2832
Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr
    930             935             940

aag gaa ccc aaa ctc aca ccg ctg tcg gaa att tct cag aga ctc ctt     2880
Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu
945             950             955                 960

aaa ctg tac tcg gat aaa ttt ggt tct gaa aat gtc aaa atg ata cag     2928
Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln
            965             970             975

gat tct ggc aag gtc aac cct aag gat ctg gat tct aag tat gca tac     2976
Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr
        980             985             990

atc cag gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag ttg caa     3024
Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln
        995             1000            1005

gaa agg aaa aca gag ttt gag aga tcc cac aac atc cgc cgc ttc atg     3072
Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met
    1010            1015            1020

ttt gag atg cca ttt acg cag acc ggg aag agg cag ggc ggg gtg gaa     3120
Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu
1025            1030            1035            1040

gag cag tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc ttc cct     3168
Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro
            1045            1050            1055

tat gtg aag aag cgc atc cct gtc atg tac cag cac cac act gac ctg     3216
Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr Asp Leu
            1060            1065            1070

aac ccc atc gag gtg gcc att gac gag atg agt aag aag gtg gcg gag     3264
Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu
        1075            1080            1085

ctc cgg cag ctg tgc tcc tcg gcc gag gtg gac atg atc aaa ctg cag     3312
Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln
    1090            1095            1100

ctc aaa ctc cag ggc agc gtg agt gtt cag gtc aat gct ggc cca cta     3360
Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly Pro Leu
1105            1110            1115            1120

gca tat gcg cga gct ttc tta gat gat aca aac aca aag cga tat cct     3408
Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro
            1125            1130            1135

gac aat aaa gtg aag ctg ctt aag gaa gtt ttc agg caa ttt gtg gaa     3456
Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu
            1140            1145            1150

gct tgc ggt caa gcc tta gcg gta aac gaa cgt ctg att aaa gaa gac     3504
Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp
        1155            1160            1165
```

```
cag ctc gag tat cag gaa gaa atg aaa gcc aac tac agg gaa atg gcg    3552
Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala
    1170             1175                 1180

aag gag ctt tct gaa atc atg cat gag cag atc tgc ccc ctg gag gag    3600
Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu
1185             1190                 1195                 1200

aag acg agc gtc tta ccg aat tcc ctt cac atc ttc aac gcc atc agt    3648
Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser
            1205                 1210                 1215

ggg act cca aca agc aca atg gtt cac ggg atg acc agc tcg tct tcg    3696
Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser Ser Ser
            1220                 1225                 1230

gtc gtg tga                                                        3705
Val Val
```

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<210> 4
<211> 1234
<212> PRT
<213> Homo sapiens
<223> Human cadherin-like asymmetry protein 2B
      (CLASP-2B)

<400> 4
Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn
1               5                   10                  15

Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val
            20                  25                  30

Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu
        35                  40                  45

Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala
    50                  55                  60

Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
65                  70                  75                  80

Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
                85                  90                  95

Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys
            100                 105                 110

Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg
        115                 120                 125

Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val
        130                 135                 140

Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu
145                 150                 155                 160

Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys
            165                 170                 175
```

16

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Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr
            180               185             190

Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
        195             200             205

Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu
    210             215             220

Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp
225             230             235                 240

Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
            245             250             255

Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
            260             265             270

Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
        275             280             285

Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
    290             295             300

Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
305             310             315                 320

Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
            325             330             335

Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
            340             345             350

Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp
        355             360             365

Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr
    370             375             380

Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile
385             390             395                 400

Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser
            405             410             415

Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val
            420             425             430

Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met
        435             440             445

Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr
    450             455             460

Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile
465             470             475                 480

Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
            485             490             495
```

Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser
            500   505   510

Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg
            515   520   525

Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser
            530   535   540

Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala
545   550   555   560

Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu
                565   570   575

Phe Thr Leu Ala Phe Lys Leu Leu Ala Asp His Gly His Asn Pro Leu
            580   585   590

Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln
            595   600   605

Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile
    610   615   620

Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala
625   630   635   640

Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser
                645   650   655

Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn
            660   665   670

Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val
            675   680   685

Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu
    690   695   700

Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser
705   710   715   720

Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu
            725   730   735

Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu
            740   745   750

His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala
            755   760   765

Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser
            770   775   780

Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met
785   790   795   800

Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys
                805   810   815

Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn

18

Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val
        835   840   845

His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp
        850   855   860

Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys
865   870   875   880

Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala
                885   890   895

His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val
                900   905   910

Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe
        915   920   925

Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr
        930   935   940

Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu
945   950·   955   960

Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln
                965   970   975

Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr
                980   985   990

Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln
        995   1000   1005

Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met
        1010   1015   1020

Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu
1025   1030   1035   1040

Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro
                1045   1050   1055

Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr Asp Leu
                1060   1065   1070

Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu
                1075   1080   1085

Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln
        1090   1095   1100

Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly Pro Leu
1105   1110   1115   1120

Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro
                1125   1130   1135

Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu
                1140   1145   1150

```
Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp
        1155                1160                1165

Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala
        1170                1175                1180

Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu
1185                1190                1195                1200

Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser
                1205                1210                1215

Gly Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser Ser Ser
                1220                1225                1230

Val Val
```

```
<210> 5
<211> 1250
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (2)..(784)

<220>
<223> Human cadherin-like asymmetry protein 2C
      (CLASP-2C)

<400> 5
g ttt aga caa gga tgc acc gcc ttc agg gtc att acc cca aac atc gac   49
  Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile Asp
    1               5                   10                  15

gag gag gcc tcc atg atg gaa gac gtg ggg atg cag gat gtc cat ttc   97
Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His Phe
            20                  25                  30

aac gag gat gtg ctg atg gag ctc ctt gag cag tgc gca gat gga ctc   145
Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu
        35                  40                  45

tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc tac aaa ctt atc   193
Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile
    50                  55                  60

atc ccc att tat gag aag cgg agg gat ttt gag agg ctg gcc cat ctg   241
Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu
65                  70                  75                  80

tat gac acg ctg cac cgg gcc tac agc aaa gtg acc gag gtc atg cac   289
Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His
                85                  90                  95

tcg ggc cgc agg ctt ctg ggg acc tac ttc cgg gta gcc ttc ttc ggg   337
Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly
```

20

```
cag gga ttc ttt gaa gat gaa gat gga aag gag tat att tac aag gaa   385
Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu
        115                 120                 125
```

```
ccc aaa ctc aca ccg ctg tcg gaa att tct cag aga ctc ctt aaa ctg   433
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
    130                 135                 140
```

```
tac tcg gat aaa ttt ggt tct gaa aat gtc aaa atg aca cag gat tct   481
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
145                 150                 155                 160
```

```
ggc aag gtc aac cct aag gat ctg gat tct aag tat gca tac atc cag   529
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
                165                 170                 175
```

```
gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag ttg caa gaa agg   577
Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg
                180                 185                 190
```

```
aaa aca gag ttt gag aga tcc cac aac atc cgc cgc ttc atg ttt gag   625
Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu
            195                 200                 205
```

```
atg cca ttt acg cag acc ggg aag agg cag ggc ggg gtg gaa gag cag   673
Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln
    210                 215                 220
```

```
tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc ttc cct tat gtg   721
Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val
225                 230                 235                 240
```

```
aag aag cgc atc cct ttc atg tac cag cac cac act gac ctg aac ccc   769
Lys Lys Arg Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro
                245                 250                 255
```

```
atc gag gtc cat tga cgagatgagt aagaaggtgg cggagctccg gcagctgtgc   824
Ile Glu Val His
            260
```

```
tcctcggccg aggtggacat gatcaaactg cagctcaaac tccagggcag cgtgagtgtt  884

caggtcaatg ctggcccact agcatatgcg cgagctttct tagatgatac aaacacaaag  944

cgatatcctg acaataaagt gaagctgctt aaggaagttt tcaggcaatt tgtggaagct 1004

tgcggtcaag ccttagcggt aaacgaacgt ctgattaaag aagaccagct cgagtatcag 1064

gaagaaatga aagccaacta cagggaaatg gcgaaggagc tttctgaaat catgcatgag 1124

cagatctgcc ccctggagga gaagacgagc gtcttaccga attcccttca catcttcaac 1184

gccatcagtg ggactccaac aagcacaatg gttcacggga tgaccagctc gtcttcggtc 1244

gtgtga                                                            1250
```

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<210> 6
<211> 260
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<212> PRT
<213> Homo sapiens
<223> Human cadherin-like asymmetry protein 2C
       (CLASP-2C)

<400> 6
Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile Asp
 1   5   10   15
Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His Phe
            20   25   30
Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu
        35   40   45
Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile
    50   55   60
Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu
65   70   75   80
Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His
                85   90   95
Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly
            100   105   110
Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu
        115   120   125
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
    130   135   140
Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
145   150   155   160
Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
                165   170   175
Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg
                180   185   190
Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu
            195   200   205
Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln
    210   215   220
Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val
225   230   235   240
Lys Lys Arg Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro
                245   250   255
Ile Glu Val His
            260

<210> 7
<211> 5862
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(4602)

<220>
<223> Human cadherin-like asymmetry protein 2D
       (CLASP-2D) KIAA1058

<400> 7
gca tct gga aat ctt gac aaa aat gcc aga ttt tct gcc atc tac agg   48
Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
 1   5   10   15

22

```
caa gac agc aat aag cta tcc aat gat gac atg ctc aag tta ctt gca    96
Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
            20              25              30

gac ttt cgg aaa cct gag aag atg gct aag ctc cca gtg att tta ggc   144
Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
        35              40              45

aat cta gac att aca att gat aat gtt tcc tca gac ttc cct aat tat   192
Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
        50              55              60

gtt aat tca tca tac att ccc aca aaa caa ttt gaa acc tgc agt aaa   240
Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
65              70              75              80

act ccc atc acg ttt gaa gtg gag gaa ttt gtg ccc tgc ata cca aaa   288
Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
                85              90              95

cac act cag cct tac acc atc tac acc aat cac ctt tac gtt tat cct   336
His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
            100             105             110

aag tac ttg aaa tac gac agt cag aag tct ttt gcc aag gct aga aat   384
Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
            115             120             125

att gcg att tgc att gaa ttc aaa gat tca gat gag gaa gac tct cag   432
Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
        130             135             140

ccc ctt aag tgc att tat ggc aga cct ggt ggg cca gtt ttc aca aga   480
Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
145             150             155             160

agc gcc ttt gct gca gtt tta cac cat cac caa aac cca gaa ttt tat   528
Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
            165             170             175

gat gag att aaa ata gag ttg ccc act cag ctg cat gaa aag cac cac   576
Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
            180             185             190

ctg ttg ctc aca ttc ttc cat gtc agc tgt gac aac tca agt aaa gga   624
Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
            195             200             205

agc acg aag aag agg gat gtc gtt gaa acc caa gtt ggc tac tcc tgg   672
Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
            210             215             220

ctt ccc ctc ctg aaa gac gga agg gtg gtg aca agc gag cag cac atc   720
Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
225             230             235             240

ccg gtc tcg gcg aac ctt cct tcg ggc tat ctt ggc tac cag gag ctt   768
Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
            245             250             255

ggg atg ggc agg cat tat ggt ccg gaa att aaa tgg gta gat gga ggc   816
```

23

```
Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly
            260                 265             270

aag cca ctg ctg aaa att tcc act cat ctg gtt tct aca gtg tat act   864
Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
        275             280             285

cag gat cag cat tta cat aat ttt ttc cag tac tgt cag aaa acc gaa   912
Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
    290             295             300

tct gga gcc caa gcc tta gga aac gaa ctt gta aag tac ctt aag agt   960
Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
305             310             315             320

ctg cat gcg atg gaa ggc cac gtg atg atc gcc ttc ttg ccc act atc   1008
Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
                325             330             335

cta aac cag ctg ttc cga gtc ctc acc aga gcc aca cag gaa gaa gtc   1056
Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
            340             345             350

gcg gtt aac gtg act cgg gtc att att cat gtg gtt gcc cag tgc cat   1104
Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
            355             360             365

gag gaa gga ttg gag agc cac ttg agg tca tat gtt aag tac gcg tat   1152
Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
    370             375             380

aag gct gag cca tat gtt gcc tct gaa tac aag aca gtg cat gaa gaa   1200
Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
385             390             395             400

ctg acc aaa tcc atg acc acg att ctc aag cct tct gcc gat ttc ctc   1248
Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu
            405             410             415

acc agc aac aaa cta ctg aag tac tca tgg ttt ttc ttt gat gta ctg   1296
Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Asp Val Leu
            420             425             430

atc aaa tct atg gct cag cat ttg ata gag aac tcc aaa gtt aag ttg   1344
Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu
            435             440             445

ctg cga aac cag aga ttt cct gca tcc tat cat cat gca gtg gaa acc   1392
Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
    450             455             460

gtt gta aat atg ctg atg cca cac atc act cag aag ttt cga gat aat   1440
Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
465             470             475             480

cca gag gca tct aag aac gcg aat cat agc ctt gct gtc ttc atc aag   1488
Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
                485             490             495

aga tgt ttc acc ttc atg gac agg ggc ttt gtc ttc aag cag atc aac   1536
Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
```

24

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aac tac att agc tgt ttt gct cct gga gac cca aag acc ctc ttt gaa     1584
Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu
        515                     520                     525

tac aag ttt gaa ttt ctc cgt gta gtg tgc aac cat gaa cat tat att     1632
Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile
    530                     535                     540

ccg ttg aac tta cca atg cca ttt gga aaa ggc agg att caa aga tac     1680
Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr
545                     550                     555                     560

caa gac ctc cag ctt gac tac tca tta aca gat gag ttc tgc aga aac     1728
Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn
                    565                 570                     575

cac ttc ttg gtg gga ctg tta ctg agg gag gtg ggg aca gcc ctc cag     1776
His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
                580                     585                     590

gag ttc cgg gag gtc cgt ctg atc gcc atc agt gtg ctc aag aac ctg     1824
Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
            595                     600                     605

ctg ata aag cat tct ttt gat gac aga tat gct tca agg agc cat cag     1872
Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln
        610                     615                     620

gca agg ata gcc acc ctc tac ctg cct ctg ttt ggt ctg ctg att gaa     1920
Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu
625                     630                     635                     640

aac gtc cag cgg atc aat gtg agg gat gtg tca ccc ttc cct gtg aac     1968
Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn
                    645                 650                     655

gcg ggc atg act gtg aag gat gaa tcc ctg gct cta cca gct gtg aat     2016
Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn
                660                     665                     670

ccg ctg gtg acg ccg cag aag gga agc acc ctg gac aac agc ctg cac     2064
Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His
            675                     680                     685

aag gac ctg ctg ggc gcc atc tcc ggc att gct tct cca tat aca acc     2112
Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr
        690                     695                     700

tca act cca aac atc aac agt gtg aga aat gct gat tcg aga gga tct     2160
Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser
705                     710                     715                     720

ctc ata agc aca gat tcg ggt aac agc ctt cca gaa agg aat agt gag     2208
Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu
                    725                 730                     735

aag agc aat tcc ctg gat aag cac caa caa agt agc aca ttg gga aat     2256
Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn
                740                     745                     750
```

```
tcc gtg gtt cgc tgt gat aaa ctt gac cag tct gag att aag agc cta    2304
Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu
        755             760             765

ctg atg tgt ttc ctc tac atc tta aag agc atg tct gat gat gct ttg    2352
Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu
    770             775             780

ttt aca tat tgg aac aag gct tca aca tct gaa ctt atg gat ttt ttt    2400
Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe
785             790             795             800

aca ata tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga    2448
Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg
            805             810             815

tac ata gcc aga aca gga atg atg cat gcc aga ttg cag cag ctg ggc    2496
Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly
            820             825             830

agc ctg gat aac tct ctc act ttt aac cac agc tat ggc cac tcg gac    2544
Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
        835             840             845

gca gat gtt ctg cac cag tca tta ctt gaa gcc aac att gct act gag    2592
Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
    850             855             860

gtt tgc ctg aca gct ctg gac acg ctt tct cta ttt aca ttg gcg ttt    2640
Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
865             870             875             880

aag aac cag ctc ctg gcc gac cat gga cat aat cct ctc atg aaa aaa    2688
Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
            885             890             895

gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag tct gaa acg    2736
Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
        900             905             910

gct tta aaa aat gtc ttc act gcc tta agg tcc tta att tat aag ttt    2784
Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
        915             920             925

ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg gct ctg tgt    2832
Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
    930             935             940

tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc atc agg acg    2880
Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
945             950             955             960

gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac ttt gat tac    2928
Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
            965             970             975

act gga aag aag tcc ttt gtc cgg aca cat ttg caa gtc atc ata tct    2976
Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
            980             985             990
```

26

```
gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gga acc aga ttc    3024
Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
        995                 1000                1005

cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt gac cgg ctt    3072
Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
    1010                1015                1020

att aag cac acc agc ttc tcc tct gat gtg aag gac tta acc aaa agg    3120
Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
1025                1030                1035                1040

ata cgc acg gtg cta atg gcc acc gcc cag atg aag gag cat gag aac    3168
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
                1045                1050                1055

gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc aaa tcc tat    3216
Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
            1060                1065                1070

gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc atg gcc agg    3264
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
        1075                1080                1085

atc cat gtc aaa aat ggc gat ctc tca gag gca gca atg tgc tat gtc    3312
Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
        1090                1095                1100

cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa gaa gca gtc    3360
His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
1105                1110                1115                1120

cag tgg gag ccg ccc ctt ctc ccc cac agc cat agc gcc tgc ctg agg    3408
Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
                1125                1130                1135

agg agc cgg gga ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc    3456
Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
            1140                1145                1150

att acc cca aac atc gac gag gag gcc tcc atg atg gaa gac gtg ggg    3504
Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
        1155                1160                1165

atg cag gat gtc cat ttc aac gag gat gtg ctg atg gag ctc ctt gag    3552
Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
    1170                1175                1180

cag tgc gca gat gga ctc tgg aaa gcc gag cgc tac gag ctc att gcc    3600
Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
1185                1190                1195                1200

gac atc tac aaa ctt atc atc ccc att tat gag aag cgg agg gat ttt    3648
Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
                1205                1210                1215

gag agg ctg gcc cat ctg tat gac acg ctg cac cgg gcc tac agc aaa    3696
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
            1220                1225                1230

gtg acc gag gtc atg cac tcg ggc cgc agg ctt ctg ggg acc tac ttc    3744
```

27

```
Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
      1235              1240                1245


cgg gta gcc ttc ttc ggg cag gca gcg caa tac cag ttt aca gac agt    3792
Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
   1250              1255                1260


gaa aca gat gtg gag gga ttc ttt gaa gat gaa gat gga aag gag tat    3840
Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
1265              1270                1275                1280


att tac aag gaa ccc aaa ctc aca ccg ctg tcg gaa att tct cag aga    3888
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
                 1285              1290                1295


ctc ctt aaa ctg tac tcg gat aaa ttt ggt tct gaa aat gtc aaa atg    3936
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
         1300              1305                1310


ata cag gat tct ggc aag gtc aac cct aag gat ctg gat tct aag tat    3984
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
         1315              1320                1325


gcc tac atc cag gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag    4032
Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
         1330              1335                1340


ttg caa gaa agg aaa aca gag ttt gag aga tcc cac aac atc cgc cgc    4080
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
1345              1350                1355                1360


ttc atg ttt gag atg cca ttt acg cag acc ggg aag agg cag ggc ggg    4128
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
                 1365              1370                1375


gtg gaa gag cag tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc    4176
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
         1380              1385                1390


ttc cct tat gtg aag aag cgc atc cct gtc atg tac cag cac cac act    4224
Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
         1395              1400                1405


gac ctg aac ccc atc gag gtg gcc att gac gag atg agt aag aag gtg    4272
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
         1410              1415                1420


gcg gag ctc cgg cag ctg tgc tcc tcg gcc gag gtg gac atg atc aaa    4320
Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
1425              1430                1435                1440


ctg cag ctc aaa ctc cag ggc agc gtg agt gtt cag gtc aat gct ggc    4368
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
                 1445              1450                1455


cca cta gca tat gcg cga gct ttc tta gat gat aca aac aca aag cga    4416
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
         1460              1465                1470


tat cct gac aat aaa gtg aag ctg ctt aag gaa gtt ttc agg caa ttt    4464
Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
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28

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gtg gaa gct tgc ggt caa gcc tta gcg gta aac gaa cgt ctg att aaa   4512
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
    1490            1495                1500

gaa gac cag ctc gag tat cag gaa gaa atg aaa gcc aac tac agg gaa   4560
Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
1505            1510                1515                1520

atg gcg aag gag ctt tct gaa atc atg cat gag cag ctg gga           4602
Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
            1525            1530
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tgatctgccc cctggaggag aagacgagcg tcttaccgaa ttcccttcac atcttcaacg 4662

ccatcagtgg gactccaaca agcacaatgg ttcacgggat gaccagctcg tcttcggtcg 4722

tgtgattaca tctcatggcc cgtgtgtggg gacttgcttt gtcatttgca aactcaggat 4782

gctttccaaa gccaatcact ggggagaccg agcacaggga ggaccagggg aaggggagag 4842

aaaggaaata aagaacaacg ttatttctta acagactttc tataggagtt gtaagaaggt 4902

gcacatattt ttttaaatct cactggcaat attcaaagtt ttcattgtgt cttaacaaag 4962

gtgtggtaga cactcttgag ctggacttag attttattct tccttgcaga gtagtgttag 5022

aatagatggc ctacagaaaa aaaaggttct gggatctaca tggcagggag ggctgcactg 5082

acattgatgc ctgggggacc ttttgcctcg aggctgagct ggaaaatctt gaaaatattt 5142

ttttttcct gtggcacatt caggttgaat acaagaacta tttttgtgac tagtttttga 5202

tgacctaagg gaactgacca ttgtaatttt tgtaccagtg aaccaggaga tttagtgctt 5262

ttatattcat ttccttgcat ttaagaaaat atgaaagctt aaggaattat gtgagcttaa 5322

aactagtcaa gcagtttaga accaaaggcc tatattaata accgcaacta tgctgaaaag 5382

tacaaagtag tacagtatat tgttatgtac atatcattgt taatacagtc ctggcattct 5442

gtacatatat gtattacatt tctacatttt taatactcac atgggcttat gcattaagtt 5502

taattgtgat aaatttgtgc tgttccagta tatgcaatac actttaatgt tttattcttg 5562

tacataaaaa tgtgcaatat ggagatgtat acagtcttta ctatattagg tttataaaca 5622

gttttaagaa tttcatcctt ttgccaaaat ggtggagtat gtaattggta aatcataaat 5682

cctgtggtga atggtggtgt actttaaagc tgtcaccatg ttatattttc ttttaagaca 5742

ttaatttagt aattttatat ttgggaaaat aaaggttttt aattttattt aactggaatc 5802

actgccctgc tgtaattaaa cattctgtac cacatctgta ttaaaaagac attgctgacc 5862

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<210> 8
<211> 1534
<212> PRT
<213> Homo sapiens
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<223> Human cadherin-like asymmetry protein 2D
      (CLASP-2D) KIAA1058

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Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg
 1   5   10   15

Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala
            20   25   30

Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly
        35   40   45

Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr
    50   55   60

Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys
65   70   75   80

Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys
            85   90   95

His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro
            100   105   110

Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn
        115   120   125

Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln
    130   135   140

Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg
145   150   155   160

Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr
            165   170   175

Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His
            180   185   190

Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly
        195   200   205

Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp
    210   215   220

Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile
225   230   235   240

Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu
            245   250   255

Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly
            260   265   270

Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr
        275   280   285

Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu
    290   295   300

30

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Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser
305             310             315                 320

Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile
                325             330                 335

Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val
            340             345             350

Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His
            355             360             365

Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr
    370             375             380

Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu
385             390             395                 400

Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu
            405             410             415

Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Asp Val Leu
            420             425             430

Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu
        435             440             445

Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr
    450             455             460

Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn
465             470             475                 480

Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys
            485             490             495

Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn
        500             505             510

Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu
        515             520             525

Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile
    530             535             540

Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr
545             550             555                 560

Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn
            565             570             575

His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln
            580             585             590

Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu
        595             600             605

Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln
    610             615             620

Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu
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31

Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn
              645   650   655

Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn
              660   665   670

Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His
              675   680   685

Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr
      690   695   700

Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser
705   710   715   720

Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu
              725   730   735

Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn
              740   745   750

Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu
              755   760   765

Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu
      770   775   780

Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe
785   790   795   800

Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg
              805   810   815

Tyr Ile Ala Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu Gly
              820   825   830

Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp
              835   840   845

Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu
      850   855   860

Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe
865   870   875   880

Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys
              885   890   895

Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr
              900   905   910

Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe
      915   920   925

Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys
      930   935   940

Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr
945   950   955   960

Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr
              965   970   975

Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser
              980   985   990

Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe
              995   1000   1005

Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu
       1010   1015   1020

Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg
1025   1030   1035   1040

Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn
                 1045   1050   1055

Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
              1060   1065   1070

Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg
              1075   1080   1085

Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val
       1090   1095   1100

His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val
1105   1110   1115   1120

Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg
              1125   1130   1135

Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val
       1140   1145   1150

Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly
       1155   1160   1165

Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu
  1170   1175   1180

Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala
1185   1190   1195   1200

Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe
              1205   1210   1215

Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
       1220   1225   1230

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
       1235   1240   1245

Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
   1250   1255   1260

Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
1265   1270   1275   1280

33

Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
        1285   1290   1295

Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
        1300   1305   1310

Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr
        1315   1320   1325

Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
    1330   1335   1340

Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg
1345   1350   1355   1360

Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
        1365   1370   1375

Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
        1380   1385   1390

Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
        1395   1400   1405

Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
        1410   1415   1420

Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
1425   1430   1435   1440

Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
        1445   1450   1455

Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
        1460   1465   1470

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
        1475   1480   1485

Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
    1490   1495   1500

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
1505   1510   1515   1520

Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly
        1525   1530

<210> 9
<211> 3642
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<213> Homo sapiens

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<221> CDS
<222> (1)..(3642)

<220>
<223> Human cadherin-like asymmetry protein 2E (CLASP

34

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gcg atg gaa ggc cac gtg atg atc gcc ttc ttg ccc act atc cta aac    48
Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn
 1               5                  10                  15

cag ctg ttc cga gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt    96
Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val
             20                  25                  30

aac gtg act cgg gtc att att cat gtg gtt gcc cag tgc cat gag gaa   144
Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu
         35                  40                  45

gga ttg gag agc cac ttg agg tca tat gtt aag tac gcg tat aag gct   192
Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala
     50                  55                  60

gag cca tat gtt gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc   240
Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
 65                  70                  75                  80

aaa tcc atg acc acg att ctc aag cct tct gcc gat ttc ctc acc agc   288
Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
                 85                  90                  95

aac aaa cta ctg agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa   336
Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys
             100                 105                 110

tct atg gct cag cat ttg ata gag aac tcc aaa gtt aag ttg ctg cga   384
Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg
         115                 120                 125

aac cag aga ttt cct gca tcc tat cat cat gca gcg gaa acc gtt gta   432
Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val
         130                 135                 140

aat atg ctg atg cca cac atc act cag aag ttt gga gat aat cca gag   480
Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu
145                 150                 155                 160

gca tct aag aac gcg aat cat agc ctt gct gtc ttc atc aag aga tgt   528
Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys
                 165                 170                 175

ttc acc ttc atg gac agg ggc ttt gtc ttc aag cag atc aac aac tac   576
Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr
             180                 185                 190

att agc tgt ttt gct cct gga gac cca aag acc ctc ttt gaa tac aag   624
Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
         195                 200                 205

ttt gaa ttt ctc cgt gta gtg tgc aac cat gaa cat tat att ccg ttg   672
Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu
     210                 215                 220

aac tta cca atg cca ttt gga aaa ggc agg att caa aga tac caa gac   720
Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp
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35

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ctc cag ctt gac tac tca tta aca gat gag ttc tgc aga aac cac ttc    768
Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
            245                 250                 255

ttg gtg gga ctg tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc    816
Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
            260                 265                 270

cgg gag gtc cgt ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata    864
Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
            275                 280                 285

aag cat tct ttt gat gac aga tat gct tca agg agc cat cag gca agg    912
Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
            290                 295                 300

ata gcc acc ctc tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc    960
Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
305                 310                 315                 320

cag cgg atc aat gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc   1008
Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
            325                 330                 335

atg acc gtg aag gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg   1056
Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
            340                 345                 350

gtg acg ccg cag aag gga agc acc ctg gac aac agc ctg cac aag gac   1104
Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp
            355                 360                 365

ctg ctg ggc gcc atc tcc ggc att gct tct cca tat aca acc tca act   1152
Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr
            370                 375                 380

cca aac atc aac agt gtg aga aat gct gat tcg aga gga tct ctc ata   1200
Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile
385                 390                 395                 400

agc aca gat tcg ggt aac agc ctt cca gaa agg aat agt gag aag agc   1248
Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser
            405                 410                 415

aat tcc ctg gat aag cac caa caa agt agc aca ttg gga aat tcc gtg   1296
Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val
            420                 425                 430

gtt cgc tgt gat aaa ctt gac cag tct gag att aag agc cta ctg atg   1344
Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met
            435                 440                 445

tgt ttc ctc tac atc tta aag agc atg tct gat gat gct ttg ttt aca   1392
Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr
            450                 455                 460

tat tgg aac aag gct tca aca tct gaa ctt atg gat ttt ttt aca ata   1440
Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile
465                 470                 475                 480
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tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga tac ata    1488
Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
                485                     490                 495

gcc agg aac cag gag ggg ttg gga ccc ata gtt cat gat cga aag tct    1536
Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser
            500                     505                 510

cag aca ttg cct gtt tcc cgt aac aga aca gga atg atg cat gcc aga    1584
Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg
        515                     520                 525

ttg cag cag ctg ggc agc ctg gat aac tct ctc act ttt aac cac agc    1632
Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser
    530                     535                 540

tat ggc cac tcg gac gca gat gtt ctg cac cag tca tta ctt gaa gcc    1680
Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala
545                     550                 555                 560

aac att gct act gag gtt tgc ctg aca gct ctg gac acg ctt tct cta    1728
Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu
                565                     570                 575

ttt aca ttg gcg ttt aag aac cag ctc ctg gcc gac cat gga cat aat    1776
Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn
            580                     585                 590

cct ctc atg aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa    1824
Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys
            595                     600                 605

cat cag tct gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc    1872
His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser
    610                     615                 620

tta att tat aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg    1920
Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met
625                     630                 635                 640

tgt gcg gct ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg    1968
Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu
                645                     650                 655

agc tcc atc agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg    2016
Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg
            660                     665                 670

aac aac ttt gat tac act gga aag aag tcc ttt gtc cgg aca cat ttg    2064
Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu
            675                     680                 685

caa gtc atc ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att    2112
Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile
        690                     695                 700

ggg gaa acc aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc    2160
Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala
705                     710                 715                 720
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aac agt gac cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag    2208
Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys
                725                 730                 735

gac tta acc aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg    2256
Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met
                740                 745                 750

aag gag cat gag aac gac cca gag atg ctg gtg gac ctc cag tac agc    2304
Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser
                755                 760                 765

ctg gcc aaa tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc    2352
Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu
                770                 775                 780

gac agc atg gcc agg atc cat gtc aaa aat ggc gat ctc tca gag gca    2400
Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala
785                 790                 795                 800

gca atg tgc tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca    2448
Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr
                805                 810                 815

cgg aaa ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc    2496
Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr
                820                 825                 830

cca aac atc gac gag gag gcc tcc atg atg gaa gac gtg ggg aaa gcc    2544
Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Lys Ala
                835                 840                 845

gag cgc tac gag ctc atc gcc gac atc tac aaa ctt atc atc ccc att    2592
Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro Ile
850                 855                 860

tat gag aag cgg agg gat ttt gag agg ctg gcc cat ctg tat gac acg    2640
Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu Tyr Asp Thr
865                 870                 875                 880

ctg cac cgg gcc tac agc aaa gtg acc gag gtc atg cac tcg ggc cgc    2688
Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His Ser Gly Arg
                885                 890                 895

agg ctt ctg ggg acc tac ttc cgg gta gcc ttc ttc ggg cag gga ttc    2736
Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly Gln Gly Phe
                900                 905                 910

ttt gaa gat gaa gat gga aag gag tat att tac aag gaa ccc aaa ctc    2784
Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu
                915                 920                 925

aca ccg ctg tcg gaa att tct cag aga ctc ctt aaa ctg tac tcg gat    2832
Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp
                930                 935                 940

aaa ttt ggt tct gaa aat gtc aaa atg ata cag gat tct ggc aag gtc    2880
Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val
945                 950                 955                 960

aac cct aag gat ctg gat tct aag tat gca tac atc cag gtg act cac    2928
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38

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          Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His
                      965                 970                 975

gtc atc ccc ttc ttt gac gaa aaa gag ttg caa gaa agg aaa aca gag        2976
Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu
              980                 985                 990

ttt gag aga tcc cac aac atc cgc cgc ttc atg ttt gag atg cca ttt        3024
Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe
              995                1000                1005

acg cag acc ggg aag agg cag ggc ggg gtg gaa gag cag tgc aaa cgg        3072
Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg
         1010                1015                1020

cgc acc atc ctg aca gcc ata cac tgc ttc cct tat gtg aag aag cgc        3120
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1025                1030                1035                1040

atc cct gtc atg tac cag cac cac act gac ctg aac ccc atc gag gtg        3168
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
              1045                1050                1055

gcc att gac gag atg agt aag aag gtg gcg gag ctc cgg cag ctg tgc        3216
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys
              1060                1065                1070

tcc tcg gcc gag gtg gac atg atc aaa ctg cag ctc aaa ctc cag ggc        3264
Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly
         1075                1080                1085

agc gtg agt gtt cag gtc aat gct ggc cca cta gca tat gcg cga gct        3312
Ser Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala
         1090                1095                1100

ttc tta gat gat aca aac aca aag cga tat cct gac aat aaa gtg aag        3360
Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys
1105                1110                1115                1120

ctg ctt aag gaa gtt ttc agg caa ttt gtg gaa gct tgc ggt caa gcc        3408
Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala
                   1125                1130                1135

tta gcg gta aac gaa cgt ctg att aaa gaa gac cag ctc gag tat cag        3456
Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln
              1140                1145                1150

gaa gaa atg aaa gcc aac tac agg gaa atg gcg aag gag ctt tct gaa        3504
Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu
              1155                1160                1165

atc atg cat gag cag atc tgc ccc ctg gag gag aag acg agc gtc tta        3552
Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu
         1170                1175                1180

ccg aat tcc ctt cac atc ttc aac gcc atc agt ggg act cca aca agc        3600
Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser
1185                1190                1195                1200

aca atg gtt cac ggg atg acc agc tcg tct tcg gtc gtg tga             3642
Thr Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
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39

<210> 10
<211> 1213
<212> PRT
<213> Homo sapiens
<223> Human cadherin-like asymmetry protein 2E (CLASP
      2E)

<400> 10

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Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn
 1               5                  10                  15
Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val
            20                  25                  30
Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu
        35                  40                  45
Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala
    50                  55                  60
Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr
65                  70                  75                  80
Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser
                85                  90                  95
Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys
            100                 105                 110
Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg
    115                 120                 125
Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val
    130                 135                 140
Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu
145                 150                 155                 160
Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys
                165                 170                 175
Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr
            180                 185                 190
Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys
    195                 200                 205
Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu
    210                 215                 220
Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp
225                 230                 235                 240
Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
            245                 250                 255
Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
            260                 265                 270
Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
    275                 280                 285
Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
    290                 295                 300
Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
305                 310                 315                 320
Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
            325                 330                 335
Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
            340                 345                 350
Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp
            355                 360                 365
Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr
    370                 375                 380
Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile
385                 390                 395                 400
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Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser
            405                 410                 415
Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val
            420                 425                 430
Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met
            435                 440                 445
Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr
    450                 455                 460
Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile
465                 470                 475                 480
Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
                485                 490                 495
Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser
            500                 505                 510
Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg
            515                 520                 525
Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser
    530                 535                 540
Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala
545                 550                 555                 560
Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu
                565                 570                 575
Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn
            580                 585                 590
Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys
            595                 600                 605
His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser
    610                 615                 620
Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met
625                 630                 635                 640
Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu
                645                 650                 655
Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg
            660                 665                 670
Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu
            675                 680                 685
Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile
    690                 695                 700
Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala
705                 710                 715                 720
Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys
            725                 730                 735
Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met
            740                 745                 750
Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser
            755                 760                 765
Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu
    770                 775                 780
Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala
785                 790                 795                 800
Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr
                805                 810                 815
Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr
            820                 825                 830
Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Lys Ala
            835                 840                 845
Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro Ile
    850                 855                 860
Tyr Glu Lys Arg Arg Asp Phe Glu Arg Leu Ala His Leu Tyr Asp Thr
865                 870                 875                 880
Leu His Arg Ala Tyr Ser Lys Val Thr Glu Val Met His Ser Gly Arg
```

41

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                885                    890                    895
Arg Leu Leu Gly Thr Tyr Phe Arg Val Ala Phe Phe Gly Gln Gly Phe
             900                    905                    910
Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu
         915                    920                    925
Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp
     930                    935                    940
Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val
945                    950                    955                    960
Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His
             965                    970                    975
Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu
             980                    985                    990
Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe
         995                   1000                   1005
Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg
     1010                   1015                   1020
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
1025                   1030                   1035                   1040
Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
             1045                   1050                   1055
Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys
         1060                   1065                   1070
Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly
         1075                   1080                   1085
Ser Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala
     1090                   1095                   1100
Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys
1105                   1110                   1115                   1120
Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala
             1125                   1130                   1135
Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln
         1140                   1145                   1150
Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu
         1155                   1160                   1165
Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu
     1170                   1175                   1180
Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser
1185                   1190                   1195                   1200
Thr Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
             1205                   1210
```

<210> 11
<211> 69
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Insertion of.
     69 nucleotides at position 2927 in human CLASP-2A
     found in human CLASP-2D

<400> 11
aagcagtcca gtgggagccg ccccttctcc cccacagcca tagcgcctgc ctgaggagga 60
gccggggag   69

<210> 12
<211> 22

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acids
      encoded by insertion of 69 nucleotides at position
      2927 of human CLASP-2A found in human CLASP-2D.

<400> 12
Ala Val Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys
  1   5   10   15

Leu Arg Arg Ser Arg Gly
              20

<210> 13
<211> 165
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Insertion at
      position 3153, entire sequence insertion in human
      CLASP-2D, portion of insertion in human CLASP-2B,
      2C and 2E

<400> 13
tgagaggctg gcccatctgt atgacacgct gcaccgggcc tacagcaaag tgaccgaggt 60
catgcactcg ggccgcaggc ttctgggggac ctacttccgg gtagccttct tcgggcaggc 120
agcgcaatac cagtttacag acagtgaaac agatgtggag ggatt   165

<210> 14
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acids
      encoded by entire insertion at position 3153 of
      human CLASP-2A found in human CLASP-2D

<400> 14
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
  1   5   10   15

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
              20   25   30

Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser
              35   40   45

Glu Thr Asp Val Glu Gly
          50

<210> 15
<211> 40
<212> PRT
<213> Artificial Sequence

43

<220>
<223> Description of Artificial Sequence: Amino acids
       encoded by insertion at position 3153 of human
       CLASP-2A found in human CLASP-2B, 2C and 2E

<400> 15
Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys
 1   5   10   15

Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe
            20   25   30

Arg Val Ala Phe Phe Gly Gln Gly
            35   40

<210> 16
<211> 3614
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3)..(2864)

<220>
<223> Human cadherin-like asymmetry protein 2A-80
       (CLASP-2A-80)

a26 cont

<400> 16
tc cag ctt gac tac tca tta aca gat gag ttc tgc aga aac cac ttc   47
   Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe
    1   5   10   15

ttg gtg gga ctg tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc   95
Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe
            20   25   30

cgg gag gtc cgt ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata   143
Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile
            35   40   45

aag cat tct ttt gat gac aga tat gct tca agg agc cat cag gca agg   191
Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg
        50   55   60

ata gcc acc ctc tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc   239
Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val
    65   70   75

cag cgg atc aat gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc   287
Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly
 80   85   90   95

atg acc gtg aag gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg   335
Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu
                100   105   110

gtg acg ccg cag aag gga agc acc ctg gac aac agc ctg cac aag gac   383
Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp

44

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ctg ctg ggc gcc atc tcc ggc att gct tct cca tat aca acc tca act   431
Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr
        130                 135                 140

cca aac atc aac agt gtg aga aat gct gat tcg aga gga tct ctc ata   479
Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile
        145                 150                 155

agc aca gat tcg ggt aac agc ctt cca gaa agg aat agt gag aag agc   527
Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser
160                 165                 170                 175

aat tcc ctg gat aag cac caa caa agt agc aca ttg gga aat tcc gtg   575
Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val
                180                 185                 190

gtt cgc tgt gat aaa ctt gac cag tct gag att aag agc cta ctg atg   623
Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met
            195                 200                 205

tgt ttc ctc tac atc tta aag agc atg tct gat gat gct ttg ttt aca   671
Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr
            210                 215                 220

tat tgg aac aag gct tca aca tct gaa ctt atg gat ttt ttt aca ata   719
Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile
        225                 230                 235

tct gaa gtc tgc ctg cac cag ttc cag tac atg ggg aag cga tac ata   767
Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile
240                 245                 250                 255

gcc agg aac cag gag ggg ttg gga ccc ata gtt cat gat cga aag tct   815
Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser
                260                 265                 270

cag aca ttg cct gtt tcc cgt aac aga aca gga atg atg cat gcc aga   863
Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg
                275                 280                 285

ttg cag cag ctg ggc agc ctg gat aac tct ctc act ttt aac cac agc   911
Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser
        290                 295                 300

tat ggc cac tcg gac gca gat gtt ctg cac cag tca tta ctt gaa gcc   959
Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala
        305                 310                 315

aac att gct act gag gtt tgc ctg aca gct ctg gac acg ctt tct cta   1007
Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu
320                 325                 330                 335

ttt aca ttg gcg ttt aag aac cag ctc ctg gcc gac cat gga cat aat   1055
Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn
                340                 345                 350

cct ctc atg aaa aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa   1103
Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys
        355                 360                 365
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45

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cat cag tct gaa acg gct tta aaa aat gtc ttc act gcc tta agg tcc      1151
His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser
        370                 375                 380

tta att tat aag ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg      1199
Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met
        385                 390                 395

tgt gcg gct ctg tgt tac gag att ctc aag tgc tgt aac tcc aag ctg      1247
Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu
400                 405                 410                 415

agc tcc atc agg acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg      1295
Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg
                420                 425                 430

aac aac ttt gat tac act gga aag aag tcc ttt gtc cgg aca cat ttg      1343
Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu
            435                 440                 445

caa gtc atc ata tct gtc agc cag ctg ata gca gac gtt gtt ggc att      1391
Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile
            450                 455                 460

ggg gaa acc aga ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc      1439
Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala
        465                 470                 475

aac agt gac cgg ctt att aag cac acc agc ttc tcc tct gat gtg aag      1487
Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys
480                 485                 490                 495

gac tta acc aaa agg ata cgc acg gtg cta atg gcc acc gcc cag atg      1535
Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met
                500                 505                 510

aag gag cat gag aac gac cca gag atg ctg gtg gac ctc cag tac agc      1583
Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser
                515                 520                 525

ctg gcc aaa tcc tat gcc agc acg ccc gag ctc agg aag acg tgg ctc      1631
Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu
        530                 535                 540

gac agc atg gcc agg atc cat gtc aaa aat ggc gat ctc tca gag gca      1679
Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala
        545                 550                 555

gca atg tgc tat gtc cac gta aca gcc cta gtg gca gaa tat ctc aca      1727
Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr
560                 565                 570                 575

cgg aaa ggc gtg ttt aga caa gga tgc acc gcc ttc agg gtc att acc      1775
Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr
                580                 585                 590

cca aac atc gac gag gag gcc tcc atg atg gaa gac gtg ggg atg cag      1823
Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln
        595                 600                 605
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46

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gat gtc cat ttc aac gag gat gtg ctg atg gag ctc ctt gag cag tgc      1871
Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys
        610                 615                 620

gca gat gga ctc tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc      1919
Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile
        625                 630                 635

tac aaa ctt atc atc ccc att tat gag aag cgg agg gat ttc ttt gaa      1967
Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu
640                 645                 650                 655

gat gaa gat gga aag gag tat att tac aag gaa ccc aaa ctc aca ccg      2015
Asp Glu Asp Gly Lys Glu· Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro
                660                 665                 670

ctg tcg gaa att tct cag aga ctc ctt aaa ctg tac tcg gat aaa ttt      2063
Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe
                675                 680                 685

ggt tct gaa aat gtc aaa atg ata cag gat tct ggc aag gtc aac cct      2111
Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro
                690                 695                 700

aag gat ctg gat tct aag tat gca tac atc cag gtg act cac gtc atc      2159
Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile
        705                 710                 715

ccc ttc ttt gac gaa aaa gag ttg caa gaa agg aaa aca gag ttt gag      2207
Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu
720                 725                 730                 735

aga tcc cac aac atc cgc cgc ttc atg ttt gag atg cca ttt acg cag      2255
Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln
                740                 745                 750

acc ggg aag agg cag ggc ggg gtg gaa gag cag tgc aaa cgg cgc acc      2303
Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr
                755             .       760                 765

atc ctg aca gcc ata cac tgc ttc cct tat gtg aag aag cgc atc cct      2351
Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro
                770                 775                 780

gtc atg tac cag cac cac act gac ctg aac ccc atc gag gtg gcc att      2399
Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile
        785                 790                 795

gac gag atg agt aag aag gtg gcg gag ctc cgg cag ctg tgc tcc tcg      2447
Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser
800                 805                 810                 815

gcc gag gtg gac atg atc aaa ctg cag ctc aaa ctc cag ggc agc gtg      2495
Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val
                820                 825                 830

agt gtt cag gtc aat gct ggc cca cta gca tat gcg cga gct ttc tta      2543
Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu
                835                 840                 845

gat gat aca aac aca aag cga tat cct gac aat aaa gtg aag ctg ctt      2591
```

47

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Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu
        850             855             860

aag gaa gtt ttc agg caa ttt gtg gaa gct tgc ggt caa gcc tta gcg    2639
Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
    865             870             875

gta aac gaa cgt ctg att aaa gaa gac cag ctc gag tat cag gaa gaa    2687
Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu
880             885             890             895

atg aaa gcc aac tac agg gaa atg gcg aag gag ctt tct gaa atc atg    2735
Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met
                900             905             910

cat gag cag atc tgc ccc ctg gag gag aag acg agc gtc tta ccg aat    2783
His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn
            915             920             925

tcc ctt cac atc ttc aac gcc atc agt ggg act cca aca agc aca atg    2831
Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met
            930             935             940

gtt cac ggg atg acc agc tcg tct tcg gtc gtg tgattacatc tcatggcccg    2884
Val His Gly Met Thr Ser Ser Ser Val Val
945                 950

tgtgtgggga cttgctttgt catttgcaaa ctcaggatgc tttccaaagc caatcactgg   2944

ggagaccgag cacagggagg accaagggga aggggagaga aaggaaataa agaacaacgt   3004

tatttcttaa cagactttct ataggagttg taagaaggtg cacatatttt tttaaatctc   3064

actggcaata ttcaaagttt tcattgtgtc ttaacaaagg tgtggtagac actcttgagc   3124

tggacttaga tttttattctt ccttgcagag tagtgttaga atagatggcc tacagaaaaa   3184

aaaggttctg ggatctacat ggcagggagg gctgcactga cattgatgcc tgggggacct    3244

tttgcctcga ctcgtgccgg aaatctgatc gtaatcaggg tacagaactt actagttttg    3304

tctaggagta tgttgtatga ctaggatttg tgctattatc tcattcaaca acatagagca    3364

agaatagtga gctaactgag ctagacactc aattaatccg ctactggctt caagtcagaa   3424

ctttgtcatt aatcatcgac tccgggacgg tcatatatgt attacatttc tacattttta   3484

atactcacat gggcttatgc attaagttta attgtgataa atttgtgctg gtccagtata   3544

tgcaatacac tttaatggtt tattcttgtc ataaaaatgt gcaatatgga gatgtataca   3604

agtctttact                                                          3614
```

a26
cont

<210> 17
<211> 954
<212> PRT
<213> Homo sapiens
<223> Human cadherin-like asymmetry protein 2A-80
      (CLASP-2A-80)

48

<400> 17

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Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu
 1               5                  10                  15

Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg
            20                  25                  30

Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys
            35                  40                  45

His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile
        50                  55                  60

Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln
65                  70                  75                  80

Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met
                85                  90                  95

Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val
            100                 105                 110

Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu
            115                 120                 125

Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro
    130                 135                 140

Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser
145                 150                 155                 160

Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn
                165                 170                 175

Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val
            180                 185                 190

Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys
        195                 200                 205

Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr
    210                 215                 220

Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser
225                 230                 235                 240

Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala
            245                 250                 255

Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln
            260                 265                 270

Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu
            275                 280                 285

Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr
            290                 295                 300

Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn
305                 310                 315                 320
```

49

Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe
            325   330   335

Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro
            340   345   350

Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His
            355   360   365

Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu
            370   375   380

Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys
385   390   395   400

Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser
            405   410   415

Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn
            420   425   430

Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln
            435   440   445

Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly
    450   455   460

Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn
465   470   475   480

Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp
            485   490   495

Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys
            500   505   510

Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu
            515   520   525

Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp
    530   535   540

Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala
545   550   555   560

Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg
            565   570   575

Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro
            580   585   590

Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp
            595   600   605

Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala
    610   615   620

Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr
625   630   635   640

Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp

50

Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu
        660   665   670

Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly
        675   680   685

Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys
    690   695   700

Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro
705   710   715   720

Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg
            725   730   735

Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr
            740   745   750

Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile
        755   760   765

Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val
    770   775   780

Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp
785   790   795   800

Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala
                805   810   815

Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
            820   825   830

Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp
        835   840   845

Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys
    850   855   860

Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val
865   870   875   880

Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met
            885   890   895

Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His
        900   905   910

Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser
        915   920   925

Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val
    930   935   940

His Gly Met Thr Ser Ser Ser Ser Val Val
945   950

<210> 18
<211> 526
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(525)

<220>
<223> Human cadherin-like asymmetry protein 2F
      (CLASP-2F)

<400> 18
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gct gat tcg aga gga tct ctc ata agc aca gat tcg ggt aac agc ctt    48
Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu
 1               5                  10                  15

cca gaa agg aat agt gag aag agc aat tcc ctg gat aag cac caa caa    96
Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln
                20                  25                  30

agt agc aca ttg gga aat tcc gtg gtt cgc tgt gat aaa ctt gac cag   144
Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln
            35                  40                  45

tct gag att aag agc cta ctg atg tgt ttc ctc tac atc tta aag agc   192
Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser
        50                  55                  60

atg tct gat gat gct ttg ttt aca tat tgg aac aag gct tca aca tct   240
Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser
    65                  70                  75                  80

gaa ctt atg gat ttt ttt aca ata tct gaa gtc tgc ctg cac cag ttc   288
Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe
                    85                  90                  95

cag tac atg ggg aag cga tac ata gcc agt gtg aga aag ata tca agt   336
Gln Tyr Met Gly Lys Arg Tyr Ile Ala Ser Val Arg Lys Ile Ser Ser
            100                 105                 110

gtg ctt gga att tct gta gac aat ggc tat ggc cac tcg gac gca gat   384
Val Leu Gly Ile Ser Val Asp Asn Gly Tyr Gly His Ser Asp Ala Asp
        115                 120                 125

gtt ctg cac cag tca tta ctt gaa gcc aac att gct act gag gtt tgc   432
Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys
    130                 135                 140

ctg aca gct ctg gac acg ctt tct cta ttt aca ttg gcg ttt aag aac   480
Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn
145                 150                 155                 160

cag ctc ctg gcc gac cat gga cat aat cct ctc atg aaa aaa aaa a     526
Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys Lys
                165                 170                 175
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<210> 19
<211> 175

<212> PRT
<213> Homo sapiens
<223> Human cadherin-like asymmetry protein 2F
      (CLASP-2F)

<400> 19
Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu
 1   5   10   15

Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln
                20   25   30

Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln
            35   40   45

Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser
        50   55   60

Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser
65   70   75   80

Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe
                85   90   95

Gln Tyr Met Gly Lys Arg Tyr Ile Ala Ser Val Arg Lys Ile Ser Ser
            100   105   110

Val Leu Gly Ile Ser Val Asp Asn Gly Tyr Gly His Ser Asp Ala Asp
            115   120   125

Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys
            130   135   140

Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn
145   150   155   160

Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys Lys Lys
                165   170   175

<210> 20
<211> 738
<212> PRT
<213> Rattus norvegicus

<220>
<223> Rat TRG protein

<400> 20
Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val
 1   5   10   15

Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn
                20   25   30

Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe
            35   40   45

Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu
        50   55   60

Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln
 65   70   75   80

Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys
                     85   90   95

Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu
            100   105   110

Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu
            115   120   125

Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr
    130   135   140

Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val
145   150   155   160

Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met
            165   170   175

Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro
            180   185   190

Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys
        195   200   205

Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala
    210   215   220

Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Asp Leu Ala Leu Gln
225   230   235   240

Arg Glu Pro Pro Val Phe Pro Tyr Ser His Thr Ser Cys Gln Arg Lys
            245   250   255

Ser Arg Gly Gly Met Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
            260   265   270

Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
            275   280   285

Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
    290   295   300

Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Leu Arg Ala Gly Leu Leu
305   310   315   320

Thr Ser Ile Asn Ser Ser Ser Pro Ser Met Lys Ser Gly Gly Thr Leu
            325   330   335

Glu Thr Thr His Leu Tyr Asp Thr Leu His Arg Pro Tyr Ser Lys Val
            340   345   350

Thr Glu Val Ile Thr Arg Ala Ala Gly Ser Trp Asp Leu Leu Pro Gly
            355   360   365

Gly Leu Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr
    370   375   380

54

```
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg
385             390             395             400

Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met
            405             410             415

Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe
        420             425             430

Ala Tyr Ile Gln Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
        435             440             445

Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Cys His Asn Ile Arg Arg
    450             455             460                     .

Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly
465             470             475                     480

Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys
            485             490             495

Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr
            500             505             510

Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val
        515             520             525

Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys
    530             535             540

Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly
545             550             555                     560

Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg
            565             570             575

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe
        580             585             590

Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys
    595             600             605

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu
    610             615             620

Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly
625             630             635             640

Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln
            645             650             655

Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu
            660             665             670

Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val
            675             680             685

Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln
    690             695             700

Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr

                                55
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Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile
              725   730   735

Phe Phe

<210> 21
<211> 1214
<212> PRT
<213> Homo sapiens

<220>
<223> Human CLASP-4 protein

<400> 21
Met Glu Ile Gln Val Leu Ile Arg Phe Leu Ser Val Ile Leu Met Gln
 1   5   10   15

Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile
              20   25   30

Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu
          35   40   45

Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro
          50   55   60

Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala
 65   70   75   80

Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile
              85   90   95

Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys
          100   105   110

Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His
          115   120   125

Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe
          130   135   140

Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu
145   150   155   160

Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu
              165   170   175

Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile
          180   185   190

Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe
          195   200   205

Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn
          210   215   220

Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser

56

Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu
          245   250   255

Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr
          260   265   270

Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys
          275   280   285

His Ala Phe Asp Thr Arg Tyr Gln His Lys Asn Gln Gln Ala Lys Ile
     290   295   300

Ala Gln Leu Tyr Leu Pro Phe Val Gly Leu Leu Glu Asn Ile Gln
305   310   315   320

Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn
          325   330   335

Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn
          340   345   350

Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln
          355   360   365

Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro
     370   375   380

Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr
385   390   395   400

Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp
               405   410   415

Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys
          420   425   430

Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro
          435   440   445

Gln Glu Leu Ile Asn Ile Leu Ile Leu Leu Glu Val Cys Leu Phe His
          450   455   460

Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp
465   470   475   480

Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala
               485   490   495

Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser
          500   505   510

Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu
          515   520   525

Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu
          530   535   540

Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe
545   550   555   560

57

Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys
              565   570   575

Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val
              580   585   590

Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe
              595   600   605

Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys
              610   615   620

Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn
625   630   635   640

Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr
              645   650   655

Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala
              660   665   670

Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe
              675   680   685

Gln Glu Ser Leu Phe Ile Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro
      690   695   700

Met Leu Ala Arg Ala Phe Pro Ala Glu Val Lys Asp Leu Thr Lys Arg
705   710   715   720

Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Lys
              725   730   735

Asp Pro Glu Met Leu Ile Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr
              740   745   750

Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Lys
              755   760   765

Ile His Val Lys Asn Gly Asp Phe Ser Glu Ala Ala Met Cys Tyr Val
      770   775   780

His Val Ala Ala Leu Val Ala Glu Phe Leu His Arg Lys Lys Leu Phe
785   790   795   800

Pro Asn Gly Cys Ser Ala Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu
              805   810   815

Glu Gly Ala Met Lys Glu Asp Ala Gly Met Met Asp Val His Tyr Ser
              820   825   830

Glu Glu Val Leu Leu Glu Leu Leu Glu Gln Cys Val Asn Gly Leu Trp
              835   840   845

Lys Ala Glu Arg Tyr Glu Ile Ile Ser Glu Ile Ser Lys Leu Ile Gly
850   855   860

Pro Ile Tyr Glu Asn Arg Arg Glu Phe Glu Asn Leu Thr Gln Val Tyr
865   870   875   880

58

Arg Thr Leu His Gly Ala Tyr Thr Lys Ile Leu Glu Val Met His Thr
                  885   890   895

Lys Lys Arg Leu Leu Gly Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln
            900   905   910

Ser Phe Phe Glu Glu Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
        915   920   925

Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr
    930   935   940

Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser Asp
945   950   955   960

Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val
            965   970   975

Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys
            980   985   990

Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala
        995   1000   1005

Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys
    1010   1015   1020

Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys
1025   1030   1035   1040

Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile
            1045   1050   1055

Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys
            1060   1065   1070

Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu
        1075   1080   1085

Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala
    1090   1095   1100

Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys
1105   1110   1115   1120

Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser
            1125   1130   1135

Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu
        1140   1145   1150

Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu
        1155   1160   1165

Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser
    1170   1175   1180

Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr
1185   1190   1195   1200

Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val

<210> 22
<211> 1288
<212> PRT
<213> Homo sapiens

<220>
<223> Human CLASP-1 protein

<400> 22

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Met Ser Phe Leu Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val
 1               5                  10                  15

Gln Asn Glu Glu Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro
            20                  25                  30

Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln
        35                  40                  45

Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro
    50                  55                  60

Val His Glu Asp Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn
65                  70                  75                  80

Asp Ser Pro Thr Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe
            85                  90                  95

Ala Ile Ile Leu Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys
            100                 105                 110

Ile Gln Leu Pro Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu
        115                 120                 125

Leu Asp Asn Leu Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr
    130                 135                 140

Lys Asp Ala Leu Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg
145                 150                 155                 160

Phe Leu Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys
            165                 170                 175

Met Val Asn Asn Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr
            180                 185                 190

Leu Cys Gln Tyr Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu
        195                 200                 205

His Phe Ile Pro Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp
    210                 215                 220

Pro Leu Thr Pro Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met
225                 230                 235                 240

Pro Glu Tyr Ser Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile
            245                 250                 255

Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp
```

Val Arg His Leu Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His
    275   280   285

Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala
    290   295   300

Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg
305   310   315   320

Ile Tyr Leu Lys Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln
           325   330   335

Gly Ser Arg Asp Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr
           340   345   350

Ala Ile Lys His Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val
         355   360   365

Leu Asn Ser Ile Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn
    370   375   380

His Ala Asp Ser Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser
385   390   395   400

Thr Asn Glu Lys Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro
           405   410   415

Arg Pro Leu Ala Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp
           420   425   430

Gln Ala Glu Thr Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys
         435   440   445

Thr Ile Ser Tyr Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser
    450   455   460

Pro Glu Val Ser Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn
465   470   475   480

Phe Arg Tyr Leu Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala
           485   490   495

Phe Lys Phe Val Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser
         500   505   510

Asn Pro Ser Cys Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser
         515   520   525

Thr Ser Arg His Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro
    530   535   540

Ile Ile Arg Gly Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met
545   550   555   560

Leu Asp Asn Thr Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His
         565   570   575

His Val Asp Thr Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile
         580   585   590

Leu Asp Leu Val Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln
        595   600   605

Gln Cys Asp Cys Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr
    610   615   620

Met Leu Phe Phe Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val
625   630   635   640

Phe Ala Ser Leu Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe
                645   650   655

Gln Gly Pro Ala Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys
            660   665   670

Cys Cys Asn His Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu
        675   680   685

Leu Tyr Leu Phe Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser
    690   695   700

Ile Val Arg Ser His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile
705   710   715   720

Ala Asp Ala Gly Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile
            725   730   735

Thr Asn Asn Phe Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe
            740   745   750

Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met
        755   760   765

Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val
    770   775   780

Asp Leu Gln Tyr Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu
785   790   795   800

Arg Arg Thr Trp Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly
            805   810   815

Asp Leu Ser Glu Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile
            820   825   830

Ala Glu Tyr Leu Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys
    835   840   845

Thr Ala Ser Leu Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser
    850   855   860

Leu Leu Thr Thr Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro
865   870   875   880

Ala Phe Leu Ser Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys
                885   890   895

Glu Asp Ser Gly Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val
            900   905   910

62

Glu Gln Leu Tyr Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr
        915   920   925

Glu Leu Ile Ala Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys
    930   935   940

Gln Arg Asp Phe Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg
945   950   955   960

Ser Tyr Leu Lys Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe
                965   970   975

Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu
                980   985   990

Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu
            995   1000   1005

Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly
    1010   1015   1020

Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys
1025   1030   1035   1040

Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro
            1045   1050   1055

Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met
            1060   1065   1070

His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser
            1075   1080   1085

Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile
    1090   1095   1100

Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val
1105   1110   1115   1120

Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp
            1125   1130   1135

Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu
            1140   1145   1150

Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
    1155   1160   1165

Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu
    1170   1175   1180

Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys
1185   1190   1195   1200

Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val
            1205   1210   1215

Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu
            1220   1225   1230

Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn

63

Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln
    1250   1255   1260

Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val
1265   1270   1275   1280

Ser Ile Ser Ser Ser Ala Glu Val
                1285

<210> 23
<211> 1220
<212> PRT
<213> Homo sapiens

<220>
<223> Human CLASP-3 protein

<400> 23
Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn
    1   5   10   15

Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp
                20   25   30

Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile
                35   40   45

Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly
        50   55   60

Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser
65   70   75   80

Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu
                85   90   95

Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys
                100   105   110

Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser
                115   120   125

Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met
        130   135   140

Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala
145   150   155   160

Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala
                165   170   175

Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp
                180   185   190

Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn
        195   200   205

Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys

64

Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro
225   230   235   240

Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser
                245   250   255

His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro
                260   265   270

Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser
        275   280   285

Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu
    290   295   300

Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu
305   310   315   320

Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly
                325   330   335

Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His
            340   345   350

Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala
        355   360   365

Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln
    370   375   380

Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys
385   390   395   400

Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln
            405   410   415

Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg
        420   425   430

Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr
        435   440   445

Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val
    450   455   460

Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu
465   470   475   480

Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val
                485   490   495

Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser
        500   505   510

Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala
    515   520   525

Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg
    530   535   540

65

Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu
545   550   555   560

Asn Leu Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu
              565   570   575

Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp
              580   585   590

Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu
          595   600   605

Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu
    610   615   620

Gly Gly Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser
625   630   635   640

Ala Val Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser
              645   650   655

Lys Phe Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp
              660   665   670

Leu Cys Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile
          675   680   685

Arg Ser His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe
    690   695   700

Glu Ile Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser
705   710   715   720

Leu Ser Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu
              725   730   735

Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu
          740   745   750

Leu Arg Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn
          755   760   765

Leu His Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu
    770   775   780

Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr
785   790   795   800

Gln Thr Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly
              805   810   815

Lys His Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val
          820   825   830

His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg
          835   840   845

Lys Tyr Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn
    850   855   860

66

Val Leu Glu Glu Ser Ala Val Ser Asp Asp Val Val Ser Pro Asp Glu
865   870   875   880

Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr Glu Ser Gly Leu Val Gly
              885   890   895

Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser Met Ala Gly Met Tyr Glu
          900   905   910

Ala Val Asn Glu Val Tyr Lys Val Leu Ile Pro Ile His Glu Ala Asn
          915   920   925

Arg Asp Ala Lys Lys Leu Ser Thr Ile His Gly Lys Leu Gln Glu Ala
      930   935   940

Phe Ser Lys Ile Val His Gln Ser Thr Gly Trp Glu Arg Met Phe Gly
945   950   955   960

Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp
              965   970   975

Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Ala Glu
          980   985   990

Ile Ser His Arg Leu Glu Gly Phe Tyr Gly Glu Arg Phe Gly Glu Asp
      995   1000   1005

Val Val Glu Val Ile Lys Asp Ser Asn Pro Val Asp Lys Cys Lys Leu
      1010   1015   1020

Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu Pro Tyr Phe
1025   1030   1035   1040

Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr Tyr Phe Asp Lys Asn Tyr
              1045   1050   1055

Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro Phe Thr Leu Asp Gly Arg
          1060   1065   1070

Ala His Gly Glu Leu His Glu Gln Phe Lys Arg Lys Thr Ile Leu Thr
      1075   1080   1085

Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg Val Asn Val Thr His
      1090   1095   1100

Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met
1105   1110   1115   1120

Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala Thr His Gln Asp Pro Ala
              1125   1130   1135

Asp Pro Lys Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr
              1140   1145   1150

Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile
      1155   1160   1165

Pro Ser Asp Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys
      1170   1175   1180

Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys

67

Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys
                1205   1210   1215

Leu Ser Ser Pro
            1220

<210> 24
<211> 987
<212> PRT
<213> Homo sapiens

<220>
<223> Human CLASP-5 protein

<400> 24
Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser
  1   5   10   15

Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser
                20   25   30

Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro
          35   40   45

Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu
      50   55   60

Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu
  65   70   75   80

Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys
                85   90   95

Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp
              100   105   110

Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr
          115   120   125

Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr
          130   135   140

Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr
145   150   155   160

Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu
                165   170   175

Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met
              180   185   190

Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro
          195   200   205

Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu
          210   215   220

Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln

Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu Ala Leu
             245   250   255

Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg Ala Pro
             260   265   270

Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp Lys Lys
             275   280   285

Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys Thr Lys
     290   295   300

Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala Thr Glu
305   310   315   320

Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln Ala Ser
             325   330   335

Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly Val Leu Arg Val
             340   345   350

Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr Tyr Leu Thr His
             355   360   365

Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp Leu Leu
     370   375   380

Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln Val Leu
385   390   395   400

His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala Cys Ala
             405   410   415

Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser Asn Phe
             420   425   430

Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu Val Gly
             435   440   445

Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu Arg Thr
     450   455   460

Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr Pro Phe
465   470   475   480

Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile Leu Tyr
             485   490   495

Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met Leu Met
             500   505   510

Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro Asp Leu
             515   520   525

Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys Lys Lys
     530   535   540

Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala Leu Val
545   550   555   560

Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly
                565   570   575

Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val
            580   585   590

Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly
        595   600   605

Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala
    610   615   620

Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr
625   630   635   640

Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu
            645   650   655

Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn
        660   665   670

Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe
        675   680   685

Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu
    690   695   700

Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe
705   710   715   720

Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser
            725   730   735

Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
        740   745   750

Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg
        755   760   765

Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr
770   775   780

Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln
785   790   795   800

Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile
            805   810   815

Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro
        820   825   830

Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
        835   840   845

Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val
    850   855   860

Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val
865   870   875   880

70

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Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg
              885             890             895

His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys
              900             905             910

Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg
          915             920             925

Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn
      930             935             940

Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile
945             950             955             960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe
              965             970             975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
              980             985
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<210> 25
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs A and B from CLASP-1

<400> 25
Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly
  1               5              10              15

Lys Glu Tyr Ile Tyr Lys Glu Pro
            20
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<210> 26
<211> 38
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs A and B from CLASP-2D KIAA1058

<400> 26
Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp
  1               5              10              15

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu
            20              25              30

Tyr Ile Tyr Lys Glu Pro
            35
```

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<210> 27
<211> 14
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<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif B from CLASP-2

<400> 27
Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro
 1   5   10

<210> 28
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs A and B from CLASP-6

<400> 28
Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly
 1   5   10   15

Lys Glu Tyr Ile Tyr Lys Glu Pro
              20

<210> 29
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs A and B from CLASP-4

<400> 29
Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly
 1   5   10   15

Lys Glu Tyr Ile Tyr Lys Glu Pro
              20

<210> 30
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs A and B from DOCK180

<400> 30
Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly
 1   5   10   15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
              20   25   30

72

<210> 31
<211> 31
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from DOCK2

<400> 31
Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn
 1   5   10   15

Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp
            20   25   30

<210> 32
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from DOCK3

<400> 32
Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn
 1   5   10   15

Lys Glu Tyr Val Cys Arg Gly His
            20

<210> 33
<211> 24
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from KIAA0716

<400> 33
Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn
 1   5   10   15

Lys Glu Phe Val Cys Arg Gly His
            20

<210> 34
<211> 23
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
motifs A and B from CLASP-3

73

<400> 34
Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln
  1   5   10   15

Glu Phe Val Tyr Lys Glu Pro
              20

<210> 35
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from rat TRG

<400> 35
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
  1   5   10   15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser
              20   25   30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln
          35   40   45

Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu
      50   55   60

a²⁶
cont.

<210> 36
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from CLASP-1

<400> 36
Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
  1   5   10   15

Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser
              20   25   30

Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln
          35   40   45

Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu
      50   55   60

<210> 37
<211> 60
<212> PRT
<213> Artificial Sequence

<220>

74

<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from CLASP-2

<400> 37
Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu
 1   5   10   15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Thr Gln Asp Ser
            20   25   30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln
        35   40   45

Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu
    50   55   60

<210> 38
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from CLASP-4

<400> 38
Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu
 1   5   10   15

Tyr Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser
            20   25   30

Asp Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln
        35   40   45

Val Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu
    50   55   60

<210> 39
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from CLASP-3

<400> 39
Pro Ala Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe
 1   5   10   15

Tyr Gly Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser
            20   25   30

Asn Pro Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln
        35   40   45

Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu
    50   55   60

75

<210> 40
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from KIAA0716

<400> 40
His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu
 1   5   10   15

Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr
              20   25   30

Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
        35   40   45

Ile Pro Glu Ser Gln Glu
        50

<210> 41
<211> 54
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from DOCK3

<400> 41
His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu
 1   5   10   15

Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala
              20   25   30

Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro
        35   40   45

Ile Pro Asp Tyr Val Asp
        50

<210> 42
<211> 46
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from DOCK2

<400> 42
Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn
 1   5   10   15

76

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr
            20   25   30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro
            35   40   45

<210> 43
<211> 53
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motif C from DOCK180

<400> 43
Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe
  1   5   10   15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val
            20   25   30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val
            35   40   45

Leu Asp Glu His Pro
        50

<210> 44
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from CLASP-1

<400> 44
Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg
  1   5   10   15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val
            20   25   30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn
            35   40   45

<210> 45
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from rat TRG

<400> 45
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg

77

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
                20   25   30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His
         35   40   45

<210> 46
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from CLASP-2D KIAA1058

<400> 46
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
  1   5   10   15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
                20   25   30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
         35   40   45

<210> 47
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from CLASP-2

<400> 47
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
  1   5   10   15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
                20   25   30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
         35   40   45

<210> 48
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from CLASP-6

<400> 48
Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg
  1   5   10   15

Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val
            20   25   30

His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg
        35   40

<210> 49
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from CLASP-4

<400> 49
Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg
  1   5   10   15

Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val
            20   25   30

Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln
        35   40   45

<210> 50
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from CLASP-3

<400> 50
Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg
  1   5   10   15

Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val
            20   25   30

Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala
        35   40   45

<210> 51
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from CLASP-5

<400> 51
Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg
  1   5   10   15

Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val
                20   25   30

Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala
        35   40   45

<210> 52
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from KIAA0716

<400> 52
Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp
 1   5   10   15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn
                20   25   30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys
        35   40   45

<210> 53
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from DOCK2

<400> 53
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
 1   5   10   15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
                20   25   30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
        35   40   45

<210> 54
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from DOCK3

<400> 54
Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp
 1   5   10   15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn

80

```
Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg
        35                  40                  45
```

<210> 55
<211> 45
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs D and E from DOCK180

<400> 55
```
Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp
  1           5                  10                  15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn
            20                  25                  30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu
        35                  40                  45
```

<210> 56
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from CLASP-1

<400> 56
```
Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala
  1           5                  10                  15

Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys
            20                  25                  30

Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln
        35                  40                  45

Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp
     50                  55
```

<210> 57
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from rat TRG

<400> 57
```
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
  1           5                  10                  15
```

```
Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
            20                  25                  30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
        35                  40                  45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
    50                  55
```

```
<210> 58
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from CLASP-2D KIAA1058

<400> 58
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
  1             5                  10                  15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
            20                  25                  30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
        35                  40                  45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
    50                  55
```

```
<210> 59
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from CLASP-2

<400> 59
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
  1             5                  10                  15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
            20                  25                  30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
        35                  40                  45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
    50                  55
```

```
<210> 60
<211> 58
<212> PRT
<213> Artificial Sequence
```

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
       motifs F and G from CLASP-6

<400> 60
Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala
 1   5   10   15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys
            20   25   30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln
        35   40   45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala
    50   55

<210> 61
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
       motifs F and G from CLASP-3

<400> 61
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln
 1   5   10   15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp
            20   25   30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp
        35   40   45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg
    50   55

<210> 62
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
       motifs F and G from CLASP-4

<400> 62
Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala
 1   5   10   15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser
            20   25   30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys
        35   40   45

Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu
    50   55

<210> 63
<211> 58
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from CLASP-5

<400> 63
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln
  1   5   10   15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp
               20   25   30

Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu
           35   40   45

Phe Ile Met Arg Cys Gly Glu Ala Val Glu
    50   55

<210> 64
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from KIAA0716

<400> 64
Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
  1   5   10   15

Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu
               20   25   30

Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met
           35   40   45

Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala
    50   55   60

<210> 65
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from DOCK2

<400> 65
Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly

84

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
            20   25   30

Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile
        35   40   45

Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys
    50   55   60

<210> 66
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from DOCK3

<400> 66
Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly
 1   5   10   15

Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn
            20   25   30

Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met
        35   40   45

Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala
    50   55   60

<210> 67
<211> 60
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP/DOCK
      motifs F and G from DOCK180

<400> 67
Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly
 1   5   10   15

Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg
            20   25   30

Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile
        35   40   45

Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg
    50   55   60

<210> 68
<211> 683
<212> DNA

<210> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 1.1
      sequence of bacterial artificial chromosome BAC4
      using primer HC2AS2

<220>
<221> modified_base
<222> (1)..(683)
<223> n is g, a, c, or t

<400> 68
tttctacagn gtntactcag gtatgtgctc cttcaacaaa attagcagtt gctgctctgt 60
gacaaagttt gcaccatttt gcaagaagaa aaaaatccta atgtgttata ttactatatt 120
tttactctat agatcttttt ctaaagaaag aaagtacaac tgaagtgctt atatgtattc 180
atataaatga ctagtacaag catcattttg caacagattt cccctttcat tggaggatct 240
tcttgatgtt atttgtacac gatcaatttt tagtcttaat aagatgaggc tgggtgtggt 300
ggctcacacc tgtaatccta gcattttgga ggccaaggtg ggcagatcac tttagcccag 360
gggtttgaga ccagcctggc caacatggca aaaccttgtc tctacaaaaa tacnaaaatt 420
atccaggcat ggtgatgtgt gcctgtagtc ccaactncct aggaggctag gggtaggggg 480
atttgcaaga ggctgggagg gtcaaagccc naantgagcc attggtncat gtcacttgga 540
ccccaagcnn ggggnganca agagcaaagg actnntgtnn tttanaaaaa aaaccgggct 600
accatacnna ccaacccncn nacctacccn acctttccan nttaaaanaa ggctttgnct 660
tgcanaggaa aancaaaatn ncc 683

<210> 69
<211> 673
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 1.2
      sequence of bacterial artificial chromosome BAC26
      using primer HC2AS2

<220>
<221> modified_base
<222> (1)..(673)
<223> n = g, a, c, or t

<400> 69
tctggtttct acagtgtata ctnaggtatg tgctccttna acaaaattag cagttgctgc 60
tctgtgacaa agtttgcacc attttgcaag aagaaaaaaa tcctaatgtg ttatattact 120
atatttttac tctatagatc tttttctaaa gaaagaaagt acaactgaag tgcttatatg 180
tattcatata aatgactagt acaagcatca ttttgcaaca gatttcccct ttcattggag 240
gatcttcttg atgttatttg tacacgatca attttttagtc ttaataagat gaggctgggt 300
gtggtggctc acacctgtaa tcctagcatt ttggaggcca aggtgggcag atcactttag 360
cccagggggtt tgagaccagc ctggccaaca tggcaaaacc ttgtctctac aaaaatacaa 420
aaattatcca ggcatggtga tgtgtgcctg tagtcccagc tacctaggag gctagggtag 480
ggggattgca agaggctngg aggtcaaggc ccgcagtgag ccatggtcat gtcactgcac 540
ccccagccag ggccgacagg agcaagactn ttgtntcaaa aaaaaacagn aaccaacanc 600
caacaacaac aacnaccttt cngcaaaana agcttgctnc aangaaacca aaatgncttc 660
ttnttttccc ccn 673

<210> 70
<211> 1034
<212> DNA
<213> Artificial Sequence

86

<220>
<223> Description of Artificial Sequence: Ref 1.3
      sequence of bacterial artificial chromosome BAC6
      using primer HC2AS2

<220>
<221> modified_base
<222> (1)..(1034)
<223> n = g, a, c, or t

<400> 70
agnnnnnccc nctacnccac ttttaacctt ttgaaaacac agtgtttnct caantatgcg 60
ctccttcaca tattagcagt tgctgctctg tgacatagtt gcaccattnt gcaagaagaa 120
aaaatcctaa gtgtnatatc actatatnnn tactctatag atcttntcta aagaaagaaa 180
gtcaactgat gtgcttatat gtatncatat aaatgactag tacatgcatc attttgcaac 240
agatntctcc tcacattgga ggatcttctn gangnattcg acacgatnan tattagtctn 300
aataagatga ngctggtgtg gnggtacact gnatctagca tntggangca tgtggcagac 360
acttanccnc ggtngagaca gctgtcactg ncnaactgtc tctntaaanc aaannctccg 420
cnggngatgg gctgagccag tcctagnngc tagntagnga tgnngagntg tngcacgncg 480
agngagcatg ntctgtactg actcatcagg cgncnacacg ntctgttcna aaacatacca 540
cacacactcn cacctncgca aaattgctct nnaaanatgc ttntttcaca cngntncaat 600
cnctatatnn tcttctattc tncnacgtnt nattannatc ttncnctgca naacnatncg 660
nccacctnna nnaccttang cttngtttca cgcttatagc tcccctacac ntnncagcnn 720
ttncnngtga agggccnccc gaatctacga ncatactctc tccgtatatn gcctcggtca 780
ncgccatctg ctgtntnctc ntcnctngcn nttnancngt ncgctatctc tnnnccggat 840
ccncnccata tnntnnctct acttanagcg taanntntnc ncncactant cacaacttnt 900
ncntnnaact ctatctnctc ctctctacca cctcacttac tacctnttca cncantctcc 960
ttcnctntcc actgatctcc acatagctgc tntactcgcc antttatcat atncacacnc 1020
tctacgctnn ntnt   1034

<210> 71
<211> 644
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 2.1
      sequence of bacterial artificial chromosome BAC4
      using primer HC2S1

<220>
<221> modified_base
<222> (1)..(644)
<223> n = g, a, c, or t

<400> 71
cttgtattna aagagggtct gcaggaagaa gtgtgtagtc ataaatacct cactggatat 60
tttatacagg attctaaaaa acctattagc aatagtatgc tagaaatagt cattagcttc 120
ttgaccttct tagaactgca cactctattg cactgtacag atttcaggat ggctgcaggg 180
attgatttga aaactaagga cacatttcaa taaacaatgt cttcaattga tttttagggc 240
tcctcctact tcaatgaagg acttcaggta gcttataatt acagacacag gctcaataca 300
ataaaaaaat tagtaaggca gagctttaaa aaaaaaaaag gaaaaagata attctaccag 360
agaaaggcta catggtgact tctgttacca gtaacaaccc ccgcactacc tttgggtctc 420
caggagcaaa acagctaatg tagttgttga tctgcttgaa gacaaagccc ctgtccatga 480
aggtgaaaca tctctgtgga ggaaaacaag caaaaaagtt atttcaggtc caaacatttc 540
ggaaatttgg attcaaagca ggcatttatt gctaataagt ttatccactg acataaaaaa 600
catgccttca acattgccag agcacctact ctattntagt cncn   644

87

<210> 72
<211> 725
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 3.1
      sequence of bacterial artificial chromosome BAC4
      using primer C96AS

<220>
<221> modified_base
<222> (1)..(725)
<223> n = g, a, c, or t

<400> 72
```
aatcagcaga ccaaacagag gcaggtagag ggtggctatc cttgcctgat ggctctgaaa 60
agaagacaca catggtaagt ttgacccagg attctgagaa ccgaactaag ttggtgctga 120
ccatctcctt tatttggatc cttcctataa agacagatat ttgattttag tcccaaaata 180
gagcaaaatc ttagtgctgt taccatgaat tttctaactg attactttct ttacaccact 240
taaaataaag gacattatca atgcacattc cttccattgg ggaccactca cccttgaagc 300
atatctgtca tcaaaagaat gctttatcag caggttcttg agcacactga tggcgatcag 360
acggacctcc cggaactcct ggagggctgt ccccacctcc ctnagtaaca gtcccaccaa 420
gaagtggttt ctgcagaact catctgttaa tgagtagtca agctgggagg tctgaaatga 480
ggatagaaac tactttgngt taggaaagat gcaatgctct tttgaataaa acaaacaaac 540
caaacnaaca aaaaaaaaac taagacccat ccttntgnat ttcaagccca ccctggggtn 600
ggtcaaagag atgatcagna ntttggcntt naaatgaaga aagaaatnaa ttntccaggg 660
gntgttctnc tttttagcac anggagggat nttaantgaa aaccaattta aatccaattn 720
aggng                                                           725
```

<210> 73
<211> 689
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 4.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2AS5

<220>
<221> modified_base
<222> (1)..(689)
<223> n = g, a, c, or t

<400> 73
```
ttcctttctg caaggctgtt cccgaatctg tgcttatgag agatcctctc gaatcagcat 60
ttctcacact gttgatgttt ggagttgagg ttgtatatgg agaagctaaa tggaaatcaa 120
gccaacaata aagtttttatt aagacagaac aaaataaaga tgagtactga actttaaggg 180
aaattgcttt tattgcactt attttttctg ttaggaagtt ggctcaagag ttgcattcca 240
ttacttcacc tttaaagaac caggtcatat acaatgagat aaaaagaaac tagtctgaaa 300
cattcagatg taaacatcaa ttcacttgtt agaaccacc tttgatcgct aaagactaaa 360
tgcatacctg tttcagaatg tgatagaatg aagacttaaa aaaattaaaa gataaatcca 420
cctacaacta tcaaatcaca aaattaaacc acacaacaaa cttgtagcat tcaaactggt 480
aataaacact gaggagccta cccaactctg aggggtgtca tggggtattt taaattttcg 540
aggagaacac agtgatatgt gacctcagcc agaagctgct gtttnagcag caggttggtg 600
ctatgctcct ttttgaagac atatttgtga agctgggtat tttggggggc ctgcttatga 660
taaaanggca aggtnttcaa tgnaggggn                                  689
```

<210> 74
<211> 680
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 4.2
      sequence of bacterial artificial chromosome BAC26
      using primer C2AS5

<220>
<221> modified_base
<222> (1)..(680)
<223> n = a, g, c, or t

<400> 74
```
ttcctttctg gaaggctgtt acccgaatct gtgcttatga gagatcctct cgaatcagca  60
tttctcacac tgttgatgtt tggagttgag gttgtatatg gagaagctaa atggaaatca 120
agccaacaat aaagttttat taagacagaa caaaataaag atgagtactg aactttaagg 180
gaaattgctt ttattgcact tattttttct gttaggaagt tggctcaaga gttgcattcc 240
attacttcac ctttaaagaa ccaggtcata tacaatgaga taaaaagaaa ctagtctgaa 300
acattcagat gtaaacatca attcacttgt tagaaaccac ctttgatcgc taaagactaa 360
atgcatacct gtttcagaat gtgatagaat gaagacttaa aaaaattaaa agataaatcc 420
acctacaact atcaaatcac aaaattaaac cncacaacaa acttgtagca ttcaaactgg 480
taataaaaca ctgaggagcc tacccaactt tgaggggtgt caatggggtn tttttaaatt 540
tttcgnggga nancccagtg ntatggtgac cttcacccaa gaagcttgtt tgtttnacca 600
agcnaggttg nnctntgctc cttttttagaa nacnntattt tnnnaaatnc tggnttttttt 660
nngnggcccc ctncnttnnt                                             680
```


<210> 75
<211> 686
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 5.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2S6

<220>
<221> modified_base
<222> (1)..(686)
<223> n = g, c, a, or t

<400> 75
```
ttcctggata aggtaattgc ttttacccaa cacaaatgtt tcttataatc aatggattta  60
gcccaaagta aacgtacttc atgttctagt gccttttaag tgtgaccttt tgttttttttc 120
taaaccaccc ggctgacctg gagtaggtga tgagagcttt aaggttgggg cccattcctt 180
gaagtgctct gattcctgtt tccagtacct cagatcctgg gcagggtttg cagtggagcg 240
tcttgagtga atggctctgg tgggttgaac ggggagggac tcaaaatgct gcccatctca 300
atttcctgta gtcttttat ttatttattt attttttgag acagagtctc gctctgtcgc 360
ccaggctgga gtacagcggc acgatctcaa ttnactgcaa cctccgcctc ctgggttcaa 420
acgactcctc tgcctcagcc tccccagcag ctgggaccac aggcacaagc caccaccgcc 480
cggctaattt tttgtntttt tagtagagat ggggtttcac catatttggc caggctgggc 540
tcaaactcct gacctcgtca tccgcncccct cggnctncca aagtgcttgg gattncaggc 600
ngtgagccca cttacacctn gggcaattcc ctgtnagtct tttttaccag agacaccatc 660
attcaacaca gcttttccac ccacaa                                      686
```

<210> 76

<211> 672
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 5.2
      sequence of bacterial artificial chromosome BAC26
      using primer C2S6

<220>
<221> modified_base
<222> (1)..(672)
<223> n = g, a, c, or t

<400> 76
```
tgagaagagc aatttcctgg ataaggtaat tgcttttacc caacacaaat gtttcttata 60
atcaatggat ttagcccaaa gtaaacgtac ttcatgttct agtgcctttt aagtgtgacc 120
ttttgttttt ttctaaacca cccggctgac ctggagtagg tgatgagagc tttaaggttg 180
gggcccattc cttgaagtgc tctgattcct gtttccagta cctcagatcc tgggcagggt 240
ttgcagtgga gcgtcttgag tgaatggctc tggtgggttg aacggggagg gactcaaaat 300
gctgcccatc tcaatttcct gtagtctttt tatttattta tttatttttt gagacagagt 360
ctcgctctgt cgcccaggct ggagtacagc ggcacgatct caattcactg caacctccgn 420
ctccctgggt tcaaacgact cctctgnctn agnctcccag cagcctggga accacaggct 480
cangccacca cgcccggcta attnttgtaa ttttnagtaa naaattgggg gttctcacca 540
tnttggccca agncttgggc ctaaaaacct tnctnaccnt cgncattcnc nccccnaccn 600
tgggcnctnc tcaaangngc ttggggattt ancannggcn ttaacccccc ntatcaccgt 660
ggnccttaat tt                                                    672
```

<210> 77
<211> 700
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 6.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2S7

<220>
<221> modified_base
<222> (1)..(700)
<223> n = g, a, c, or t

<400> 77
```
nagngngggt ttnagncgtt tgaagcctgn nacgnggtgn gtgctngaac tctgtgggct 60
ttcaggtact ggggtatctg ggagcctgct gtttgcattg ctagtgcatc agaccagggc 120
tttttcctcc ctgtagctgc tacttataca catagctcta actgagatga ttctccagac 180
aactgatgca gagcagcaaa agcttctgcc gttctcccct tctaggagtg tctcctttct 240
ttggaaagag atcatgaggg gctagattgt aatgaagtga ggctcagtgc ttgagcacat 300
ccggtaaaag ttccaatata ttggtcataa agtttctcat tctttatagc agttaatttc 360
tctggctcat gagtttttctt agttttaatc tgactttttaa attaatgtct ccagcaccag 420
tcatatcccc agggcaaact caaaggcatg agaggccaga ctcgggtcct ggtcatagca 480
acccctgtct agggccttgg tccctgcctc cgcttgtgtg ctgtggcgca ggtcctatgg 540
gcccttagga aacaggacca ccctgtcgca ccccctacag agaccagcca agtttgacat 600
tagatcaccg tagcaatgtn tgcaaattcc agtttcttgc taaaacaggt taagccttgc 660
agccacttta tctgtaactg gcngaggttt tgacataaaa                       700
```

<210> 78
<211> 676

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 7.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2S8

<220>
<221> modified_base
<222> (1)..(676)
<223> n = g, a, c, or t

<400> 78
ctctcgacac gctgtttcta ttaacattgg cgtttaaggt ttgtatcaat ttgctgttcg 60
nggttctagt tttacctttc acattcattc tgcttggtaa gctcagtgag cacaaactta 120
ctatgttgca tttttacttc agcaattatt tttgtccctg taaggaaacc attaatcttt 180
aaattccttt aatgaaatca ttccacagtg aatggcttga atgccctgaa ataaaattta 240
actggtcagt gtgtgctgcg cgcttgggta tggtggaaac acggtctctg gaggcagtta 300
actcttggct cgaaccttga ggatggtgaa tataggcacc taatcaggca tttctgcctt 360
gaatatcttt aaatatatcc aaatgttata gcgtttaatt agattttttat gtagaaagga 420
gcaataaaca caagacacat gttttcagtt ttttatctgt tactgcatta aatgataaaa 480
acgttttgga gatagaaaat gaaagggggtt tttttttttgt cttgtttttaa agtttttagca 540
aataatattc aagtaggtgg agatggactc ttcaccactc tcctgttttt aggaacccaa 600
tactttttca ttcttgctaa atgattactt ccatttctag catagaaaag gagaaaattg 660
gaatgagtgt ttatat 676

<210> 79
<211> 686
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 8.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2S9

<220>
<221> modified_base
<222> (1)..(686)
<223> n = a, c, g, or t

<400> 79
cgctttnaaa tnccagccgc tactgcgggg cgntnaattc gaaacgtgtt gttntctgtg 60
atgcctggct ctgattgtgt gggattggtc atcagtggcg gttggcagnt ggggttcatg 120
gaagcggcca tggggactga tggcaggccc ttggattgcc accgcagagc ctggcagtgt 180
ctttggtctg cattcctacc ggcgaagtct catttcacct cacgtgttat ctcttggaaa 240
gcattccttt agcgggctgt gtctaccctt ccatcctctc gtccaaactc cccctccttc 300
tctgttctgt ctccttccca tcctcttctc cccagttctt cttcctatgt tccttcctca 360
gtggtttctc ttcctctgtt tgactttcca aggtcatttt gactgttcct gctcccaact 420
acaaagatac taaaatctca cctaaccact cttcttcttt cttaatgaaa gaatgttttc 480
agtccatccc aaatttgtgt ggacttcaca aaccttctct aaaatggagc cttttctctt 540
cctactcttg actagntggt aaacgctcca tgttcttggc cagaactccc tggtgagtag 600
cgtcactccc actttcctgt gcagaaccaa gcctcctaga aaactccttt gcanctgagt 660
gggttgggac acgccctttn tttggg 686

<210> 80
<211> 680
<212> DNA

<210> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 9.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2AS10

<220>
<221> modified_base
<222> (1)..(680)
<223> n = g, a, t, or c

<400> 80
```
tttanaccna tntatccgng tcagttanag gagtctctga gaaatttccg acagcggtgt 60
gagtttgggt tccttgtaaa tatactcctt tccatcttca tcttcaaaga atccctgtga 120
cataaagcac aattagagct atccctgaac gtaagcccag ggcttaccac ctaggaagcg 180
ttcttttatt acaagggggga aaaaaaggaa tgggtctaaa aatccagctg aaatgggctt 240
tctgaatgag aaagaaaatg ctaataacat gaagtctagg tgcaaaggta aaggaaaaac 300
acaacattgc aaacttattc aagaatgcag tcattaagtg ttgagtgaaa tgaaagattt 360
tggatacaag actaagctgt cccagggaag tctaatggga gtcaagcctg tttcactttc 420
ccaagaagca gaactcacta naaaatgatg agcagcccac gacaggcagg ctcagaagtg 480
gacatgcctc ccttctcctg atggctncca tgcacacagg attttatggc atgaactgaa 540
gcgtttgggg gtctggagta agtttagtaa aagttaggta aagcttgtat aaattgtatt 600
tttgctttac ccgatgagaa aaaaaatatt naagacctgg tagcttcaat attcaagaaa 660
aatatttttc atntcacccg                                            680
```

<210> 81
<211> 619
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 10.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2S11

<220>
<221> modified_base
<222> (1)..(619)
<223> n = g, a, c, or t

<400> 81
```
ngnangtgga gccncgancc agggacaatc tnaacctnct taaactgtac tcggatnaat 60
ttggttctga aaatgtcaaa atgatacagg attctggcaa ggtattgacc atgtttggan 120
aagtttcata gcaatgtaat gttgtgatnc gattacatat natatatttt taaatgtnta 180
tagaaaaaaa cacangaaaa atattaagga ttgttggccc gtgagtggca ggtgtatntt 240
cttnctgatc ctttagngct ttccattaca tgcntgacat taaaaaaanc tttatcgcct 300
aatttttgaa acatctaatt ttacaaaata attaaccgtn tggccangna tattntcatt 360
tttaggncca gctatttaga aactctgaca naaatgaggg gctgtggctt ncctncctnn 420
acttgnccct ctttcnngna tgtaccacat gaacttgncn cctctttcnn ctnaccgggt 480
ggcatgttan aggacaggtt gaaaccncan tngggcngga nttnggtnna attgggacac 540
aatggtacna ngctctatng gaatngaaac tctcccnacn nncngtgnnc cntggggaaa 600
atgngncnna ttcattttn                                             619
```

<210> 82
<211> 597
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 11.1
    sequence of bacterial artificial chromosome BAC4
    using primer C2S12

<220>
<221> modified_base
<222> (1)..(597)
<223> n = g, a, c, or t

<400> 82
```
agnanngttn ngcagctgca nntctggacc canaggccgc angggcacga gccnggacac 60
gctcggcaaa gagctgtcca gagggattca gaagcttcag gactggaagg gtctttcgag 120
ctcagttagc cacccccaca cccatttcag tttcacattt atctagtgct tccttttgaa 180
tacttgggat gtttttctgt tgatctgttg gcacttcctt cttccacaag accagaagct 240
catatccaat ctaaggtcac ttacccttct gagaatctga tgaaaatggc gtgccttatg 300
tgcctagatg cttttgcaca cagtctaagg tgacttatgg actccaggtc cagcagccac 360
acccagtcct gggtctccgc acagggaggg acccgtcttc acacacctgt ctcaggttct 420
agcattgggc tgcttcagcg gtctcaggct gtgagtaaat gggatgtgag cttggatcgc 480
cccacgctgt tgnccccgg ggggcttggc cagctggcca cttngaaatg cctcctttg 540
cccaggaaag ctcactgcat ttcaatgggg nttntccacg aagttcanct ttanggg    597
```

<210> 83
<211> 634
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 12.1
    sequence of bacterial artificial chromosome BAC4
    using primer C2S13

<220>
<221> modified_base
<222> (1)..(634)
<223> n = a, c, g, or t

<400> 83
```
agnaaggtnn ctcantnaan ncagcgtgag ngttcaggtg agccaggcac agcaggccgg 60
agggcagcag gggacgtcct tgcccctggg tgacttgaga gtcgtttcca ctaacaaggt 120
ctacttgaga gcctcggttt accaagtgat ccctgctccc ttcccccaac gtntgtgaca 180
tttctcctga tatcagaggg ggaggaaacc tcatgatccc tgccccccgc cccatgagga 240
ctgactgtgg ggacaaagag ccagatctca tagactaccc tgatttgtca gtatttgggg 300
aattctgggt gcctgattag aagcatcaag actcttctaa atncaaagaa gtgtggagag 360
cagtagattt tcctataaaa ctggtgttgc tggtttctat gaaaattgga tccaaaaaaa 420
gtccttaagt ttaccctctt aatggnatct tttgattaat ggaattcatt attttaatat 480
agcccaatca atccaatttt tctttattgg tagcattttt atgttctctt taaaaaaatc 540
ttggnctacc tccaaaattt cacagatgtt ctcctagggt tttcctcctt ttggttcaag 600
catcccattc aangtcttgc agtccattct gggg                            634
```

<210> 84
<211> 567
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 13.1
    sequence of bacterial artificial chromosome BAC4
    using primer C2S14

<220>
<221> modified_base
<222> (1)..(567)
<223> n = a, g, c, or t

<400> 84
gacttanatt tattcttcct tgcagagtag tgttagaata gatggcctac agaaaaaaaa 60
ggttctggga tctacatggc agggagggct gcactgacat tgatgcctgg gggacctttt 120
gcctcgaggc tgagctggaa aatcttgaaa atattttttt tttcctgtgg cacattcagg 180
ttgaatacaa gaactatttt tgtgactatg tttttgatga cctaagggaa ctgaccattg 240
taattttgt accantgaac cangagattt aagtgctttt atattcattt ccttgcattt 300
aagaaaatat gaaagcttaa ggaattatgt gagcttaaaa ctagtcaagc antttagaac 360
caaaggccta tnttnataac cgcaactatg ctnaaaagna caaagtagta cagnatattg 420
ntatgtacat atcatttggt aatacacncc nggcnttctg tacatatatg tattacattt 480
ctacnttttt aatactcccn tgggcttatg ccnttaaggt taanttgnga taaatttngg 540
ctgttccngt ntatncnata cncttt 567

<210> 85
<211> 662
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Ref 14.1
      sequence of bacterial artificial chromosome BAC4
      using primer C2AS15

<220>
<221> modified_base
<222> (1)..(662)
<223> n = a, c, g, t

<400> 85
atgagaatgt aatacatata tgtacagaat gccaggactg tattaacaat gatatgtaca 60
taacaatata ctgtactact ttgtactttt cagcatagtt gcggttatta atataggcct 120
ttggttctaa actgcttgac tagtttttaag ctcacataat tccttaagct ttcatatttt 180
cttaaatgca aggaaatgaa tataaaagca ctaaatctcc tggttcactg gtacaaaaat 240
tacaatggtc agttcccta ggtcatcaaa aactagtcac aaaaatagtt cttgtattca 300
acctgaatgt gccacaggaa aaaaaaata ttttcaagat tttccagctc agcctcgagg 360
caaaaggccc ccaggcatca atgtcagngc agccctcctg ccatgtagat cccagaacct 420
ttttttctg taggccatct attctaacac tactctgcag ggagaataaa atctaaagnc 480
cagctcaaga gtgctaccac acctttgtta agacacaatg aaaactttgg atattggcag 540
gngagattta aaaaaaaatg tgcccttct taccactcct atagnaaagt ctggttaaga 600
aataaccgtt ggtctttatt ttccttttnt ttccccttcc cttgggnctt cctggggctc 660
gg 662

<210> 86
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: KV1.3
      inhibitor

<400> 86
Thr Thr Asn Asn Asn Pro Asn Ser Ala Val Asn Ile Lys Lys Ile Phe
1   5   10   15

94

Thr Asp Val

<210> 87
<211> 4898
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (567)..(4148)

<220>
<223> Human CLASP-2

<400> 87
aattgtaata cgactcacta tagggcgaat tgggtaccgg gccccccctc gaggtcgacg 60

gtatcgataa gcttgatatc gaattcggca cgagtttac accatcacca aaacccagaa 120

ttttatgatg agattaaaat agagttgccc actcagctgc atgaaaagca ccacctgttg 180

ctcacattct tccatgtcag ctgtgacaac tcaagtaaag gaagcacgaa gaagagggat 240

gtcgttgaaa cccaagttgg ctactcctgg cttcccctcc tgaaagacgg aagggtggtg 300

acaagcgagc agcacatccc ggtctcggcg aaccttcctt cgggctatct tggctaccaa 360

gagcttggga tgggcaggca ttatggtccg gaaattaaat gggtagatgg aggcaagcca 420

ctgctgaaaa tttccactca tctggtttct acagggatac tcaggatcag catttacata 480

attttttcca gtactgtcag aaaaccgaat ctggagccca agccttagga aacgaacttg 540

taaagtacct taagagtctg catgcg atg gaa ggc cac gtg atg atc gcc ttc 593
                                Met Glu Gly His Val Met Ile Ala Phe
                                 1   5

ttg ccc act atc cta aac cag ctg ttc cga gtc ctc acc aga gcc aca 641
Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr
 10   15   20   25

cag gaa gaa gtc gcg gtt aac gtg act cgg gtc att att cat gtg gtt 689
Gln Glu Glu Val Ala Val Asn Val Thr Arg Val Ile Ile His Val Val
                30   35   40

gcc cag tgc cat gag gaa gga ttg gag agc cac ttg agg tca tat gtt 737
Ala Gln Cys His Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val
            45   50   55

aag tac gcg tat aag gct gag cca tat gtt gcc tct gaa tac aag aca 785
Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr
            60   65   70

gtg cat gaa gaa ctg acc aaa tcc atg acc acg att ctc aag cct tct 833
Val His Glu Glu Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser
     75   80   85

gcc gat ttc ctc acc agc aac aaa cta ctg agg tac tca tgg ttt ttc 881

95

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Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe
 90              95              100             105

ttt gat gta ctg atc aaa tct atg gct cag cat ttg ata gag aac tcc    929
Phe Asp Val Leu Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser
            110             115             120

aaa gtt aag ttg ctg cga aac cag aga ttt cct gca tcc tat cat cat    977
Lys Val Lys Leu Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His
            125             130             135

gca gcg gaa acc gtt gta aat atg ctg atg cca cac atc act cag aag   1025
Ala Ala Glu Thr Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys
        140             145             150

ttt gga gat aat cca gag gca tct aag aac gcg aat cat agc ctt gct   1073
Phe Gly Asp Asn Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala
    155             160             165

gtc ttc atc aag aga tgt ttc acc ttc atg gac agg ggc ttt gtc ttc   1121
Val Phe Ile Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe
170             175             180             185

aag cag atc aac aac tac att agc tgt ttt gct cct gga gac cca aag   1169
Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys
            190             195             200

acc ctc ttt gaa tac aag ttt gaa ttt ctc cgt gta gtg tgc aac cat   1217
Thr Leu Phe Glu Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His
            205             210             215

gaa cat tat att ccg ttg aac tta cca atg cca ttt gga aaa ggc agg   1265
Glu His Tyr Ile Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg
        220             225             230

att caa aga tac caa gac ctc cag ctt gac tac tca tta aca gat gag   1313
Ile Gln Arg Tyr Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu
        235             240             245

ttc tgc aga aac cac ttc ttg gtg gga ctg tta ctg agg gag gtg ggg   1361
Phe Cys Arg Asn His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly
250             255             260             265

aca gcc ctc cag gag ttc cgg gag gtc cgt ctg atc gcc atc agt gtg   1409
Thr Ala Leu Gln Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val
            270             275                 2
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Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe
 90              95              100                     105


ttt gat gta ctg atc aaa tct atg gct cag cat ttg ata gag aac tcc   929
Phe Asp Val Leu Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser
                110             115                 120


aaa gtt aag ttg ctg cga aac cag aga ttt cct gca tcc tat cat cat   977
Lys Val Lys Leu Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His
            125             130                 135


gca gcg gaa acc gtt gta aat atg ctg atg cca cac atc act cag aag  1025
Ala Ala Glu Thr Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys
            140             145                 150


ttt gga gat aat cca gag gca tct aag aac gcg aat cat agc ctt gct  1073
Phe Gly Asp Asn Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala
            155             160                 165


gtc ttc atc aag aga tgt ttc acc ttc atg gac agg ggc ttt gtc ttc  1121
Val Phe Ile Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe
170             175             180                     185


aag cag atc aac aac tac att agc tgt ttt gct cct gga gac cca aag  1169
Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys
                190             195                 200


acc ctc ttt gaa tac aag ttt gaa ttt ctc cgt gta gtg tgc aac cat  1217
Thr Leu Phe Glu Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His
                205             210                 215


gaa cat tat att ccg ttg aac tta cca atg cca ttt gga aaa ggc agg  1265
Glu His Tyr Ile Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg
                220             225                 230


att caa aga tac caa gac ctc cag ctt gac tac tca tta aca gat gag  1313
Ile Gln Arg Tyr Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu
            235             240                 245


ttc tgc aga aac cac ttc ttg gtg gga ctg tta ctg agg gag gtg ggg  1361
Phe Cys Arg Asn His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly
250             255                 260                     265


aca gcc ctc cag gag ttc cgg gag gtc cgt ctg atc gcc atc agt gtg  1409
Thr Ala Leu Gln Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val
                270             275                 280


ctc aag aac ctg ctg ata aag cat tct ttt gat gac aga tat gct tca  1457
Leu Lys Asn Leu Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser
                285             290                 295


agg agc cat cag gca agg ata gcc acc ctc tac ctg cct ctg ttt ggt  1505
Arg Ser His Gln Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly
            300             305                 310


ctg ctg att gaa aac gtc cag cgg atc aat gtg agg gat gtg tca ccc  1553
Leu Leu Ile Glu Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro
            315             320                 325


ttc cct gtg aac gcg ggc atg acc gtg aag gat gaa tcc ctg gct cta  1601
Phe Pro Val Asn Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu
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96

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cca gct gtg aat ccg ctg gtg acg ccg cag aag gga agc acc ctg gac    1649
Pro Ala Val Asn Pro Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp
            350                355                360

aac agc ctg cac aag gac ctg ctg ggc gcc atc tcc ggc att gct tct    1697
Asn Ser Leu His Lys Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser
        365                370                375

cca tat aca acc tca act cca aac atc aac agt gtg aga aat gct gat    1745
Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp
        380                385                390

tcg aga gga tct ctc ata agc aca gat tcg ggt aac agc ctt cca gaa    1793
Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu
    395                400                405

agg aat agt gag aag agc aat tcc ctg gat aag cac caa caa agt agc    1841
Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser
410                415                420                425

aca ttg gga aat tcc gtg gtt cgc tgt gat aaa ctt gac cag tct gag    1889
Thr Leu Gly Asn Ser Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu
                430                435                440

att aag agc cta ctg atg tgt ttc ctc tac atc tta aag agc atg tct    1937
Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser
            445                450                455

gat gat gct ttg ttt aca tat tgg aac aag gct tca aca tct gaa ctt    1985
Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu
        460                465                470

atg gat ttt ttt aca ata tct gaa gtc tgc ctg cac cag ttc cag tac    2033
Met Asp Phe Phe Thr Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr
    475                480                485

atg ggg aag cga tac ata gcc agg aac cag gag ggg ttg gga ccc ata    2081
Met Gly Lys Arg Tyr Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile
490                495                500                505

gtt cat gat cga aag tct cag aca ttg cct gtt tcc cgt aac aga aca    2129
Val His Asp Arg Lys Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr
                510                515                520

gga atg atg cat gcc aga ttg cag cag ctg ggc agc ctg gat aac tct    2177
Gly Met Met His Ala Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser
            525                530                535

ctc act ttt aac cac agc tat ggc cac tcg gac gca gat gtt ctg cac    2225
Leu Thr Phe Asn His Ser Tyr Gly His Ser Asp Ala Asp Val Leu His
        540                545                550

cag tca tta ctt gaa gcc aac att gct act gag gtt tgc ctg aca gct    2273
Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala
    555                560                565

ctg gac acg ctt tct cta ttt aca ttg gcg ttt aag aac cag ctc ctg    2321
Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu
570                575                580                585
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gcc gac cat gga cat aat cct ctc atg aaa aaa gtt ttt gat gtc tac     2369
Ala Asp His Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr
            590             595                 600

ctg tgt ttt ctt caa aaa cat cag tct gaa acg gct tta aaa aat gtc     2417
Leu Cys Phe Leu Gln Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val
            605             610                 615

ttc act gcc tta agg tcc tta att tat aag ttt ccc tca aca ttc tat     2465
Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr
            620             625                 630

gaa ggg aga gcg gac atg tgt gcg gct ctg tgt tac gag att ctc aag     2513
Glu Gly Arg Ala Asp Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys
        635             640                 645

tgc tgt aac tcc aag ctg agc tcc atc agg acg gag gcc tcc cag ctg     2561
Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu
650             655                 660                 665

ctc tac ttc ctg atg agg aac aac ttt gat tac act gga aag aag tcc     2609
Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser
                670             675                 680

ttt gtc cgg aca cat ttg caa gtc atc ata tct gtc agc cag ctg ata     2657
Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile
            685                 690                 695

gca gac gtt gtt ggc att ggg gaa acc aga ttc cag cag tcc ctg tcc     2705
Ala Asp Val Val Gly Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser
            700             705                 710

atc atc aac aac tgt gcc aac agt gac cgg ctt att aag cac acc agc     2753
Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser
715                 720                 725

ttc tcc tct gat gtg aag gac tta acc aaa agg ata cgc acg gtg cta     2801
Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu
730             735                 740                 745

atg gcc acc gcc cag atg aag gag cat gag aac gac cca gag atg ctg     2849
Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met Leu
                750             755                 760

gtg gac ctc cag tac agc ctg gcc aaa tcc tat gcc agc acg ccc gag     2897
Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu
            765             770                 775

ctc agg aag acg tgg ctc gac agc atg gcc agg atc cat gtc aaa aat     2945
Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys Asn
            780             785                 790

ggc gat ctc tca gag gca gca atg tgc tat gtc cac gta aca gcc cta     2993
Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala Leu
            795             800                 805

gtg gca gaa tat ctc aca cgg aaa ggc gtg ttt aga caa gga tgc acc     3041
Val Ala Glu Tyr Leu Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr
810             815                 820                 825
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gcc ttc agg gtc att acc cca aac atc gac gag gag gcc tcc atg atg     3089
Ala Phe Arg Val Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met
                830             835                 840

gaa gac gtg ggg atg cag gat gtc cat ttc aac gag gat gtg ctg atg     3137
Glu Asp Val Gly Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met
            845                 850                 855

gag ctc ctt gag cag tgc gca gat gga ctc tgg aaa gcc gag cgc tac     3185
Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr
        860                 865                 870

gag ctc atc gcc gac atc tac aaa ctt atc atc ccc att tat gag aag     3233
Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys
    875                 880                 885

cgg agg gat ttc ttt gaa gat gaa gat gga aag gag tat att tac aag     3281
Arg Arg Asp Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys
890                 895                 900                 905

gaa ccc aaa ctc aca ccg ctg tcg gaa att tct cag aga ctc ctt aaa     3329
Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys
                910                 915                 920

ctg tac tcg gat aaa ttt ggt tct gaa aat gtc aaa atg ata cag gat     3377
Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp
            925                 930                 935

tct ggc aag gtc aac cct aag gat ctg gat tct aag tat gca tac atc     3425
Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile
            940                 945                 950

cag gtg act cac gtc atc ccc ttc ttt gac gaa aaa gag ttg caa gaa     3473
Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu
955                 960                 965

agg aaa aca gag ttt gag aga tcc cac aac atc cgc cgc ttc atg ttt     3521
Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe
970                 975                 980                 985

gag atg cca ttt acg cag acc ggg aag agg cag ggc ggg gtg gaa gag     3569
Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu
                990                 995                 1000

cag tgc aaa cgg cgc acc atc ctg aca gcc ata cac tgc ttc cct tat     3617
Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr
            1005                1010                1015

gtg aag aag cgc atc cct gtc atg tac cag cac cac act gac ctg aac     3665
Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn
        1020                1025                1030

ccc atc gag gtg gcc att gac gag atg agt aag aag gtg gcg gag ctc     3713
Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu
    1035                1040                1045

cgg cag ctg tgc tcc tcg gcc gag gtg gac atg atc aaa ctg cag ctc     3761
Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu
1050                1055                1060                1065

aaa ctc cag ggc agc gtg agt gtt cag gtc aat gct ggc cca cta gca     3809
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99

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Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala
            1070                1075                1080

tat gcg cga gct ttc tta gat gat aca aac aca aag cga tat cct gac    3857
Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp
            1085                1090                1095

aat aaa gtg aag ctg ctt aag gaa gtt ttc agg caa ttt gtg gaa gct    3905
Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala
        1100                1105                1110

tgc ggt caa gcc tta gcg gta aac gaa cgt ctg att aaa gaa gac cag    3953
Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln
        1115                1120                1125

ctc gag tat cag gaa gaa atg aaa gcc aac tac agg gaa atg gcg aag    4001
Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys
1130                1135                1140                1145

gag ctt tct gaa atc atg cat gag cag atc tgc ccc ctg gag gag aag    4049
Glu Leu Ser Glu Ile Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys
            1150                1155                1160

acg agc gtc tta ccg aat tcc ctt cac atc ttc aac gcc atc agt ggg    4097
Thr Ser Val Leu Pro Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly
            1165                1170                1175

act cca aca agc aca atg gtt cac ggg atg acc agc tcg tct tcg gtc    4145
Thr Pro Thr Ser Thr Met Val His Gly Met Thr Ser Ser Ser Ser Val
        1180                1185                1190
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gtg tgattacatc tcatggcccg tgtgtgggga cttgctttgt catttgcaaa   4198
Val

ctcaggatgc tttccaaagc caatcactgg ggagaccgag cacagggagg accaaggga 4258

aggggagaga aaggaaataa agaacaacgt tatttcttaa cagactttct ataggagttg 4318

taagaaggtg cacatatttt tttaaatctc actggcaata ttcaaagttt tcattgtgtc 4378

ttaacaaagg tgtggtagac actcttgagc tggacttaga ttttattctt ccttgcagag 4438

tagtgttaga atagatggcc tacagaaaaa aaaggttctg ggatctacat ggcagggagg 4498

gctgcactga cattgatgcc tgggggacct tttgcctcga ctcgtgccgg aaatctgatc 4558

gtaatcaggg tacagaactt actagttttg tctaggagta tgttgtatga ctaggatttg 4618

tgctattatc tcattcaaca acatagagca agaatagtga gctaactgag ctagacactc 4678

aattaatccg ctactggctt caagtcagaa ctttgtcatt aatcatcgac tccgggacgg 4738

tcatatatgt attacatttc tacatttta atactcacat gggcttatgc attaagttta   4798

attgtgataa atttgtgctg gtccagtata tgcaatacac tttaatggtt tattcttgtc 4858

ataaaaatgt gcaatatgga gatgtataca agtctttact   4898

<210> 88
<211> 1194

                                        100

<212> PRT
<213> Homo sapiens
<223> Human CLASP-2

<400> 88
Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln
 1   5   10   15

Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn
            20   25   30

Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly
            35   40   45

Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu
        50   55   60

Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys
65   70   75   80

Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn
                85   90   95

Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser
            100   105   110

Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn
            115   120   125

Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn
        130   135   140

Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala
145   150   155   160

Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe
                165   170   175

Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile
            180   185   190

Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe
            195   200   205

Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn
        210   215   220

Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu
225   230   235   240

Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu
                245   250   255

Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg
            260   265   270

Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys
        275   280   285

His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile
        290   295   300

101

Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln
305   310   315   320

Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met
                325   330   335

Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val
            340   345   350

Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu
        355   360   365

Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro
    370   375   380

Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser
385   390   395   400

Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn
            405   410   415

Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val
        420   425   430

Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys
        435   440   445

Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr
    450   455   460

Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser
465   470   475   480

Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala
            485   490   495

Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln
        500   505   510

Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu
        515   520   525

Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr
    530   535   540

Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn
545   550   555   560

Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe
            565   570   575

Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro
        580   585   590

Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His
        595   600   605

Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu
    610   615   620

102

Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys
625   630   635   640

Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser
            645   650   655

Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn
            660   665   670

Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln
            675   680   685

Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly
    690   695   700

Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn
705   710   715   720

Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp
            725   730   735

Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys
            740   745   750

Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu
        755   760   765

Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp
    770   775   780

Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala
785   790   795   800

Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg
            805   810   815

Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro
            820   825   830

Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp
        835   840   845

Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala
    850   855   860

Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr
865   870   875   880

Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp
            885   890   895

Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu
            900   905   910

Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly
        915   920   925

Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys
    930   935   940

Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro

103

```
945                    950                  955                    960

Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg
            965                  970                  975

Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr
            980                  985                  990

Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile
            995                  1000                 1005

Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val
    1010                  1015                 1020

Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp
1025                  1030                 1035                 1040

Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala
            1045                 1050                 1055

Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser
            1060                 1065                 1070

Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp
    1075                  1080                 1085

Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys
    1090                  1095                 1100

Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val
1105                  1110                 1115                 1120

Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met
            1125                 1130                 1135

Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His
            1140                 1145                 1150

Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser
            1155                 1160                 1165

Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val
    1170                  1175                 1180

His Gly Met Thr Ser Ser Ser Ser Val Val
1185                  1190
```

<210> 89
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Furin cleavage
      consensus sequence

<400> 89
Arg Lys Gln Arg
  1

```
<210> 90
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   Human CLASP-2
      predicted cleavage site by homology

<400> 90
Arg Asn Gln Arg
  1


<210> 91
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
      consensus motif E

<220>
<221> MOD_RES
<222> (3)
<223> Xaa = any amino acid

<220>
<221> MOD_RES
<222> (6)
<223> Xaa = any amino acid

<400> 91
Pro Glu Xaa Ala Ile Xaa Met
  1               5


<210> 92
<211> 15
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Conserved
      consensus motif F

<220>
<221> MOD_RES
<222> (1)..(15)
<223> Xaa is any amino acid.

<400> 92
Leu Xaa Met Xaa Leu Gly Xaa Val Xaa Xaa Xaa Val Asn Xaa Gly
  1               5                  10                  15


<210> 93
<211> 125
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a76
cont.

105

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: CLASP-2C exon
      not found in CLASP-2A

<220>
<221> misc_feature
<222> (1)..(125)
<223> N is A, C, G, or T.

<400> 93
agggattttg agaggctggc ccatctgtat gacacgctgc accgggccta cagcaaagtg   60
accgaggtca tgcactcggg ccgcagttnc tggggaccta cttccgggta gccttcttcg   120
ggcag   125

<210> 94
<211> 44
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Amino acids
      encoded by CLASP-2C exon not found in CLASP-2A

<400> 94
Arg Asp Phe Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala
 1   5   10   15

Tyr Ser Lys Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly
            20   25   30

Thr Tyr Phe Arg Val Ala Phe Phe Gly Gln Gly Phe
            35   40

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer F1

<400> 95
cccagatttt tatgatgag   19

<210> 96
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer R1

<400> 96

gataatgaca aagttctgac   20

<210> 97
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer F2

<400> 97
ctggaaatct tgacaaaaat gc   22

<210> 98
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer R2

<400> 98
gtctttttaa tacagatgtg g   21

<210> 99
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer F3

<400> 99
gagaggctgg cccatctgta tg   22

<210> 100
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer R3

<400> 100
atcttcaaag aatccctgcc   20

<210> 101
<211> 21
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Exemplary
      probe/primer F4

<400> 101
gaagcagtcc agtgggagcc g   21

<210> 102
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer R4

<400> 102
gcctccccgg ctcctcctca gg   22

<210> 103
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer R5

<400> 103
cctccacatc tgtttcactg tc   22

<210> 104
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer F5

<400> 104
ctccatgatg gaagacgtgg g   21

<210> 105
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer R6

<400> 105
gatgagctcg tagcgctcgg c   21

<210> 106
<211> 20

108

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer F6

<400> 106
cattggcgtt taagctcctg   20

<210> 107
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer F7

<400> 107
ggacccatag ttcatgatcg   20

<210> 108
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Exemplary
      probe/primer R4

<400> 108
cttcatcttc aagaaatccc tc   22

<210> 109
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
      oligo 1

<400> 109
gaaggcgatc atcacgtggc cttccatcgc   30

<210> 110
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
      oligo 2

<400> 110
gcttcaagta atgactggtg cagaacatct g   31

```
<210> 111
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
      oligo 3

<400> 111
gctcctcctc aggcaggcgc tatggctgtg g                               31


<210> 112
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
      oligo 4

<400> 112
gtaggcccgg tgcagcgtgt catacagatg g                               31


<210> 113
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
      oligo 5

<400> 113
gcaatgtctg agactttcga tcatgaacta tg                              32


<210> 114
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Antisense
      oligo 6

<400> 114
caggagctgg ttcttaaa                                              18


<210> 115
<211> 81
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 1A
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026
cont.

<400> 115
gcaggggaaa aacctggccc catgattcac ttacttccca ccggatctct cccatgacac 60
gtgaggatta ttacaattta a   81

<210> 116
<211> 118
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 1B

<400> 116
ttatcccttt actacttgcg aagtgagttc ggtagatggg agtggagaag agaaccttag 60
aatcattgtt tagtcttcat ctttcacagc tcaggctgaa ggcctttcct tgctgaga   118

<210> 117
<211> 42
<212> DNA
<213> Homo sapiens

<220>
<223> Exon 1C

<400> 117
gcggcagagc gtgtctgagg tggtgcgcgg ctccgtgctc ct   42

<210> 118
<211> 6791
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (102)..(6044)

<220>
<223> Human CLASP-2 gene

<400> 118
ggcaaagcca aagctaattg agcaagctaa ttgagccact cgactatgaa aatgtcatcg 60

tccagaagaa gactcagatc ctgaacgact gtttacggga g atg ctg ctc ttc cct 116
                                             Met Leu Leu Phe Pro
                                             1   5

tac gat gac ttt cag acg gcc atc ctg aga cga cag ggt cga tac ata   164
Tyr Asp Asp Phe Gln Thr Ala Ile Leu Arg Arg Gln Gly Arg Tyr Ile
                10   15   20

tgc tca aca gtg cct gcg aag gcg gaa gag gaa gca cag agc ttg ttt   212
Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu Ala Gln Ser Leu Phe
            25   30   35

gtt aca gag tgc atc aaa acc tat aac tct gac tgg cat ctt gtg aac   260
Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp Trp His Leu Val Asn
        40   45   50

111

```
tat aaa tat gaa gat tac tca gga gag ttt cga cag ctt ccg aac aaa    308
Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg Gln Leu Pro Asn Lys
        55                  60                  65

gtg gtc aag ttg gat aaa ctt cca gtt cat gtc tat gaa gtt gac gag    356
Val Val Lys Leu Asp Lys Leu Pro Val His Val Tyr Glu Val Asp Glu
70                  75                  80                  85

gag gtc gac aaa gat gag gat gct gcc tcc ctt ggt tcc cag aag ggt    404
Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu Gly Ser Gln Lys Gly
                90                  95                  100

ggg atc acc aag cat ggc tgg ctg tac aaa ggc aac atg aac agt gcc    452
Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly Asn Met Asn Ser Ala
                105                 110                 115

atc agc gtg acc atg agg tca ttt aag aga cga ttt ttc cac ctg att    500
Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg Phe Phe His Leu Ile
        120                 125                 130

caa ctt ggc gat gga tcc tat aat ttg aat ttt tat aaa gat gaa aag    548
Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe Tyr Lys Asp Glu Lys
        135                 140                 145

atc tcc aaa gaa cca aaa gga tca ata ttt ctg gat tcc tgt atg ggt    596
Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu Asp Ser Cys Met Gly
150                 155                 160                 165

gtc gtt cag aac aac aaa gtc agg cgt ttt gct ttt gag ctc aag atg    644
Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala Phe Glu Leu Lys Met
                170                 175                 180

cag gac aaa agt agt tat ctc ttg gca gca gac agt gaa gtg gaa atg    692
Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp Ser Glu Val Glu Met
                185                 190                 195

gaa gaa tgg atc aca att cta aat aag atc ctc cag ctc aac ttt gaa    740
Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu Gln Leu Asn Phe Glu
                200                 205                 210

gct gca atg caa gaa aag cga aat ggc gac tct cac gaa gat gat gaa    788
Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser His Glu Asp Asp Glu
        215                 220                 225

caa agc aaa ttg gaa ggt tct ggt tcc ggt tta gat agc tac ctg ccg    836
Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu Asp Ser Tyr Leu Pro
230                 235                 240                 245

gaa ctt gcc aag agt gca aga gaa gca gaa atc aaa cta aaa agt gaa    884
Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile Lys Leu Lys Ser Glu
                250                 255                 260

agc aga gtc aaa ctt ttt tat ttg gac cca gat gcc cag aag ctt gac    932
Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp Ala Gln Lys Leu Asp
                265                 270                 275

ttc tca tca gct gag cca gaa gtg aag tca ttt gaa gag aag ttt gga    980
Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe Glu Glu Lys Phe Gly
                280                 285                 290
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112

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aaa agg atc ctt gtc aag tgc aat gat tta tct ttc aat ttg caa tgc    1028
Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser Phe Asn Leu Gln Cys
    295             300             305

tgt gtt gcc gaa aat gaa gaa gga ccc act aca aat gtt gaa cct ttc    1076
Cys Val Ala Glu Asn Glu Glu Gly Pro Thr Thr Asn Val Glu Pro Phe
310             315             320             325

ttt gtt act cta tcc ctg ttt gac ata aaa tac aac cgg aag att tct    1124
Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr Asn Arg Lys Ile Ser
            330             335             340

gcc gat ttc cac gta gac ctg aac cat ttc tca gtg agg caa atg ctc    1172
Ala Asp Phe His Val Asp Leu Asn His Phe Ser Val Arg Gln Met Leu
            345             350             355

gcc acc acg tcc ccg gcg ctg atg aat ggc agt ggg cag agc cca tct    1220
Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser Gly Gln Ser Pro Ser
        360             365             370

gtc ctc aag ggc atc ctt cat gaa gcc gcc atg cag tat ccg aag cag    1268
Val Leu Lys Gly Ile Leu His Glu Ala Ala Met Gln Tyr Pro Lys Gln
    375             380             385

gga ata ttt tca gtc act tgt cct cat cca gat ata ttt ctt gtg gcc    1316
Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp Ile Phe Leu Val Ala
390             395             400             405

aga att gaa aaa gtc ctt cag ggg agc atc aca cat tgc gct gag cca    1364
Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr His Cys Ala Glu Pro
            410             415             420

tat atg aaa agt tca gac tct tct aag gtg gcc cag aag gtg ctg aag    1412
Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala Gln Lys Val Leu Lys
            425             430             435

aat gcc aag cag gca tgc caa aga cta gga cag tat aga atg cca ttt    1460
Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln Tyr Arg Met Pro Phe
        440             445             450

gct tgg gca gca agg aca ttg ttt aag gat gca tct gga aat ctt gac    1508
Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala Ser Gly Asn Leu Asp
455             460             465

aaa aat gcc aga ttt tct gcc atc tac agg caa gac agc aat aag cta    1556
Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln Asp Ser Asn Lys Leu
470             475             480             485

tcc aat gat gac atg ctc aag tta ctt gca gac ttt cgg aaa cct gag    1604
Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp Phe Arg Lys Pro Glu
            490             495             500

aag atg gct aag ctc cca gtg att tta ggc aat cta gac att aca att    1652
Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn Leu Asp Ile Thr Ile
            505             510             515

gat aat gtt tcc tca gac ttc cct aat tat gtt aat tca tca tac att    1700
Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val Asn Ser Ser Tyr Ile
            520             525             530

ccc aca aaa caa ttt gaa acc tgc agt aaa act ccc atc acg ttt gaa    1748
```

113

```
Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys Thr Pro Ile Thr Phe Glu
    535             540             545

gtg gag gaa ttt gtg ccc tgc ata cca aaa cac act cag cct tac acc    1796
Val Glu Glu Phe Val Pro Cys Ile Pro Lys His Thr Gln Pro Tyr Thr
550             555             560             565

atc tac acc aat cac ctt tac gtt tat cct aag tac ttg aaa tac gac    1844
Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro Lys Tyr Leu Lys Tyr Asp
                570             575             580

agt cag aag tct ttt gcc aag gct aga aat att gcg att tgc att gaa    1892
Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn Ile Ala Ile Cys Ile Glu
            585             590             595

ttc aaa gat tca gat gag gaa gac tct cag ccc ctt aag tgc att tat    1940
Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln Pro Leu Lys Cys Ile Tyr
            600             605             610

ggc aga cct ggt ggg cca gtt ttc aca aga agc gcc ttt gct gca gtt    1988
Gly Arg Pro Gly Gly Pro Val Phe Thr Arg Ser Ala Phe Ala Ala Val
    615             620             625

tta cac cat cac caa aac cca gaa ttt tat gat gag att aaa ata gag    2036
Leu His His His Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile Glu
630             635             640             645

ttg ccc act cag ctg cat gaa aag cac cac ctg ttg ctc aca ttc ttc    2084
Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe Phe
            650             655             660

cat gtc agc tgt gac aac tca agt aaa gga agc acg aag aag agg gat    2132
His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg Asp
            665             670             675

gtc gtt gaa acc caa gtt ggc tac tcc tgg ctt ccc ctc ctg aaa gac    2180
Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys Asp
    680             685             690

gga agg gtg gtg aca agc gag cag cac atc ccg gtc tcg gcg tac ctt    2228
Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Tyr Leu
    695             700             705

cct tcg ggc cat ctt ggc tac caa gag ctt ggg atg ggc agg cat tat    2276
Pro Ser Gly His Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His Tyr
710             715             720             725

ggt ccg gaa att aaa tgg gta gat gga ggc aag cca ctg ctg aaa att    2324
Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys Ile
                730             735             740

tcc act cat ctg gtt tct aca gtg tat act cag gat cag cat tta cat    2372
Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu His
            745             750             755

aat ttt ttc cag tac tgt cag aaa acc gaa tct gga gcc caa gcc tta    2420
Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala Leu
            760             765             770

gga aac gaa ctt gta aag tac ctt aag agt ctg cat gcg atg gaa ggc    2468
Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu Gly
```

114

cac gtg atg atc gcc ttc ttg ccc act atc cta aac cag ctg ttc cga   2516
His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe Arg
790   795   800   805

gtc ctc acc aga gcc aca cag gaa gaa gtc gcg gtt aac gtg act cgg   2564
Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr Arg
                   810   815   820

gtc att att cat gtg gtt gcc cag tgc cat gag gaa gga ttg gag agc   2612
Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu Ser
                   825   830   835

cac ttg agg tca tat gtt aag tac gcg tat aag gct gag cca tat gtt   2660
His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr Val
                   840   845   850

gcc tct gaa tac aag aca gtg cat gaa gaa ctg acc aaa tcc atg acc   2708
Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met Thr
                   855   860   865

acg att ctc aag cct tct gcc gat ttc ctc acc agc aac aaa cta ctg   2756
Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu Leu
870   875   880   885

agg tac tca tgg ttt ttc ttt gat gta ctg atc aaa tct atg gct cag   2804
Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala Gln
                   890   895   900

cat ttg ata gag aac tcc aaa gtt aag ttg ctg cga aac cag aga ttt   2852
His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg Phe
                   905   910   915

cct gca tcc tat cat cat gca gcg gaa acc gtt gta aat atg ctg atg   2900
Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu Met
                   920   925   930

cca cac atc act cag aag ttt gga gat aat cca gag gca tct aag aac   2948
Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys Asn
935   940   945

gcg aat cat agc ctt gct gtc ttc atc aag aga tgt ttc acc ttc atg   2996
Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe Thr Phe Met
950   955   960   965

gac agg ggc ttt gtc ttc aag cag atc aac aac tac att agc tgt ttt   3044
Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys Phe
                   970   975   980

gct cct gga gac cca aag acc ctc ttt gaa tac aag ttt gaa ttt ctc   3092
Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe Leu
                   985   990   995

cgt gta gtg tgc aac cat gaa cat tat att ccg ttg aac tta cca atg   3140
Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met
               1000   1005   1010

cca ttt gga aaa ggc agg att caa aga tac caa gac ctc cag ctt gac   3188
Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu Asp
               1015   1020   1025

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tac tca tta aca gat gag ttc tgc aga aac cac ttc ttg gtg gga ctg    3236
Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly Leu
1030                1035                1040                1045

tta ctg agg gag gtg ggg aca gcc ctc cag gag ttc cgg gag gtc cgt    3284
Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg Glu Val Arg
                1050                1055                1060

ctg atc gcc atc agt gtg ctc aag aac ctg ctg ata aag cat tct ttt    3332
Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser Phe
                1065                1070                1075

gat gac aga tat gct tca agg agc cat cag gca agg ata gcc acc ctc    3380
Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile Ala Thr Leu
                1080                1085                1090

tac ctg cct ctg ttt ggt ctg ctg att gaa aac gtc cag cgg atc aat    3428
Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln Arg Ile Asn
    1095                1100                1105

gtg agg gat gtg tca ccc ttc cct gtg aac gcg ggc atg acc gtg aag    3476
Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met Thr Val Lys
1110                1115                1120                1125

gat gaa tcc ctg gct cta cca gct gtg aat ccg ctg gtg acg ccg cag    3524
Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val Thr Pro Gln
                1130                1135                1140

aag gga agc acc ctg gac aac agc ctg cac aag gac ctg ctg ggc gcc    3572
Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu Leu Gly Ala
                1145                1150                1155

atc tcc ggc att gct tct cca tat aca acc tca act cca aac atc aac    3620
Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile Asn
    1160                1165                1170

agt gtg aga aat gct gat tcg aga gga tct ctc ata agc aca gat tcg    3668
Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp Ser
    1175                1180                1185

ggt aac agc ctt cca gaa agg aat agt gag aag agc aat tcc ctg gat    3716
Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu Asp
1190                1195                1200                1205

aag cac caa caa agt agc aca ttg gga aat tcc gtg gtt cgc tgt gat    3764
Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys Asp
                1210                1215                1220

aaa ctt gac cag tct gag att aag agc cta ctg atg tgt ttc ctc tac    3812
Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu Tyr
                1225                1230                1235

atc tta aag agc atg tct gat gat gct ttg ttt aca tat tgg aac aag    3860
Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn Lys
    1240                1245                1250

gct tca aca tct gaa ctt atg gat ttt ttt aca ata tct gaa gtc tgc    3908
Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val Cys
    1255                1260                1265
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ctg cac cag ttc cag tac atg ggg aag cga tac ata gcc agg aac cag      3956
Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn Gln
1270            1275            1280            1285

gag ggg ttg gga ccc ata gtt cat gat cga aag tct cag aca ttg cct      4004
Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu Pro
         1290            1295            1300

gtt tcc cgt aac aga aca gga atg atg cat gcc aga ttg cag cag ctg      4052
Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln Leu
         1305            1310            1315

ggc agc ctg gat aac tct ctc act ttt aac cac agc tat ggc cac tcg      4100
Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His Ser
         1320            1325            1330

gac gca gat gtt ctg cac cag tca tta ctt gaa gcc aac att gct act      4148
Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala Thr
      1335            1340            1345

gag gtt tgc ctg aca gct ctg gac acg ctt tct cta ttt aca ttg gcg      4196
Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu Ala
1350            1355            1360            1365

ttt aag aac cag ctc ctg gcc gac cat gga cat aat cct ctc atg aaa      4244
Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met Lys
         1370            1375            1380

aaa gtt ttt gat gtc tac ctg tgt ttt ctt caa aaa cat cag tct gaa      4292
Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu
         1385            1390            1395

acg gct tta aaa aat gtc ttc act gcc tta agg tcc tta att tat aag      4340
Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys
         1400            1405            1410

ttt ccc tca aca ttc tat gaa ggg aga gcg gac atg tgt gcg gct ctg      4388
Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp Met Cys Ala Ala Leu
   1415            1420            1425

tgt tac gag att ctc aag tgc tgt aac tcc aag ctg agc tcc atc agg      4436
Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg
1430            1435            1440            1445

acg gag gcc tcc cag ctg ctc tac ttc ctg atg agg aac aac ttt gat      4484
Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp
         1450            1455            1460

tac act gga aag aag tcc ttt gtc cgg aca cat ttg caa gtc atc ata      4532
Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His Leu Gln Val Ile Ile
         1465            1470            1475

tct gtc agc cag ctg ata gca gac gtt gtt ggc att ggg gaa acc aga      4580
Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Glu Thr Arg
         1480            1485            1490

ttc cag cag tcc ctg tcc atc atc aac aac tgt gcc aac agt gac cgg      4628
Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg
      1495            1500            1505

ctt att aag cac acc agc ttc tcc tct gat gtg aag gac tta acc aaa      4676
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117

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Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys
1510          1515          1520          1525

agg ata cgc acg gtg cta atg gcc acc gcc cag atg aag gag cat gag    4724
Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu
              1530          1535          1540

aac gac cca gag atg ctg gtg gac ctc cag tac agc ctg gcc aaa tcc    4772
Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser
          1545          1550          1555

tat gcc agc acg ccc gag ctc agg aag acg tgg ctc gac agc atg gcc    4820
Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala
          1560          1565          1570

agg atc cat gtc aaa aat ggc gat ctc tca gag gca gca atg tgc tat    4868
Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr
      1575          1580          1585

gtc cac gta aca gcc cta gtg gca gaa tat ctc aca cgg aaa ggc gtg    4916
Val His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Gly Val
1590          1595          1600          1605

ttt aga caa gga tgc acc gcc ttc agg gtc att acc cca aac atc gac    4964
Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile Thr Pro Asn Ile Asp
              1610          1615          1620

gag gag gcc tcc atg atg gaa gac gtg ggg atg cag gat gtc cat ttc    5012
Glu Glu Ala Ser Met Met Glu Asp Val Gly Met Gln Asp Val His Phe
              1625          1630          1635

aac gag gat gtg ctg atg gag ctc ctt gag cag tgc gca gat gga ctc    5060
Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln Cys Ala Asp Gly Leu
          1640          1645          1650

tgg aaa gcc gag cgc tac gag ctc atc gcc gac atc tac aaa ctt atc    5108
Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp Ile Tyr Lys Leu Ile
          1655          1660          1665

atc ccc att tat gag aag cgg agg gat ttc ttt gaa gat gaa gat gga    5156
Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe Glu Asp Glu Asp Gly
1670          1675          1680          1685

aag gag tat att tac aag gaa ccc aaa ctc aca ccg ctg tcg gaa att    5204
Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile
              1690          1695          1700

tct cag aga ctc ctt aaa ctg tac tcg gat aaa ttt ggt tct gaa aat    5252
Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn
              1705          1710          1715

gtc aaa atg ata cag gat tct ggc aag gtc aac cct aag gat ctg gat    5300
Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp
          1720          1725          1730

tct aag tat gca tac atc cag gtg act cac gtc atc ccc ttc ttt gac    5348
Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp
      1735          1740          1745

gaa aaa gag ttg caa gaa agg aaa aca gag ttt gag aga tcc cac aac    5396
Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn
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118

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atc cgc cgc ttc atg ttt gag atg cca ttt acg cag acc ggg aag agg   5444
Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg
                1770                1775                1780

cag ggc ggg gtg gaa gag cag tgc aaa cgg cgc acc atc ctg aca gcc   5492
Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala
                1785                1790                1795

ata cac tgc ttc cct tat gtg aag aag cgc atc cct gtc atg tac cag   5540
Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln
            1800                1805                1810

cac cac act gac ctg aac ccc atc gag gtg gcc att gac gag atg agt   5588
His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser
        1815                1820                1825

aag aag gtg gcg gag ctc cgg cag ctg tgc tcc tcg gcc gag gtg gac   5636
Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp
1830                1835                1840                1845

atg atc aaa ctg cag ctc aaa ctc cag ggc agc gtg agt gtt cag gtc   5684
Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val
                1850                1855                1860

aat gct ggc cca cta gca tat gcg cga gct ttc tta gat gat aca aac   5732
Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn
                1865                1870                1875

aca aag cga tat cct gac aat aaa gtg aag ctg ctt aag gaa gtt ttc   5780
Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe
            1880                1885                1890

agg caa ttt gtg gaa gct tgc ggt caa gcc tta gcg gta aac gaa cgt   5828
Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg
    1895                1900                1905

ctg att aaa gaa gac cag ctc gag tat cag gaa gaa atg aaa gcc aac   5876
Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn
1910                1915                1920                1925

tac agg gaa atg gcg aag gag ctt tct gaa atc atg cat gag cag atc   5924
Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Ile
                1930                1935                1940

tgc ccc ctg gag gag aag acg agc gtc tta ccg aat tcc ctt cac atc   5972
Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His Ile
            1945                1950                1955

ttc aac gcc atc agt ggg act cca aca agc aca atg gtt cac ggg atg   6020
Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly Met
        1960                1965                1970

acc agc tcg tct tcg gtc gtg tga ttacatctca tggcccgtgt gtggggactt   6074
Thr Ser Ser Ser Ser Val Val
        1975                1980

gctttgtcat ttgcaaactc aggatgcttt ccaaagccaa tcactgggga gaccgagcac   6134

agggaggacc aaggggaagg ggagagaaag gaaataaaga acaacgttat ttcttaacag   6194
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actttctata ggagttgtaa gaaggtgcac atatttttt aaatctcact ggcaatattc 6254

aaagttttca ttgtgtctta acaaaggtgt ggtagacact.cttgagctgg acttagattt 6314

tattcttcct tgcagagtag tgttagaata gatggcctac agaaaaaaaa ggttctggga 6374

tctacatggc agggagggct gcactgacat tgatgcctgg gggacctttt gcctcgactc 6434

gtgccggaaa tctgatcgta atcagggtac agaacttact agttttgtct aggagtatgt 6494

tgtatgacta ggatttgtgc tattatctca ttcaacaaca tagagcaaga atagtgagct 6554

aactgagcta gacactcaat taatccgcta ctggcttcaa gtcagaactt tgtcattaat 6614

catcgactcc gggacggtca tatatgtatt acatttctac atttttaata ctcacatggg 6674

cttatgcatt aagtttaatt gtgataaatt tgtgctggtc cagtatatgc aatacacttt 6734

aatggtttat tcttgtcata aaaatgtgca atatggagat gtatacaagt ctttact      6791
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Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu
            20                  25                  30
Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp
         35                  40                  45
Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg
      50                  55                  60
Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val
 65                  70                  75                  80
Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu
               85                  90                  95
Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly
            100                 105                 110
Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg
         115                 120                 125
Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe
      130                 135                 140
Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu
145                 150                 155                 160
Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala
               165                 170                 175
Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp
            180                 185                 190
Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu
            195                 200                 205
Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser
         210                 215                 220
His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu
225                 230                 235                 240
Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile
               245                 250                 255
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Lys Leu Lys Ser Glu Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp
            260                 265                 270
Ala Gln Lys Leu Asp Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe
            275                 280                 285
Glu Glu Lys Phe Gly Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser
    290                 295                 300
Phe Asn Leu Gln Cys Cys Val Ala Glu Asn Glu Glu Gly Pro Thr Thr
305                 310                 315                 320
Asn Val Glu Pro Phe Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr
                325                 330                 335
Asn Arg Lys Ile Ser Ala Asp Phe His Val Asp Leu Asn His Phe Ser
            340                 345                 350
Val Arg Gln Met Leu Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser
            355                 360                 365
Gly Gln Ser Pro Ser Val Leu Lys Gly Ile Leu His Glu Ala Ala Met
    370                 375                 380
Gln Tyr Pro Lys Gln Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp
385                 390                 395                 400
Ile Phe Leu Val Ala Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr
                405                 410                 415
His Cys Ala Glu Pro Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala
            420                 425                 430
Gln Lys Val Leu Lys Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln
            435                 440                 445
Tyr Arg Met Pro Phe Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala
    450                 455                 460
Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln
465                 470                 475                 480
Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp
            485                 490                 495
Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn
            500                 505                 510
Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val
    515                 520                 525
Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys Thr
    530                 535                 540
Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys His
545                 550                 555                 560
Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro Lys
                565                 570                 575
Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn Ile
            580                 585                 590
Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln Pro
        595                 600                 605
Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg Ser
    610                 615                 620
Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp
625                 630                 635                 640
Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu
            645                 650                 655
Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser
            660                 665                 670
Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu
    675                 680                 685
Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro
    690                 695                 700
Val Ser Ala Tyr Leu Pro Ser Gly His Leu Gly Tyr Gln Glu Leu Gly
705                 710                 715                 720
Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys
            725                 730                 735
Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln
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121

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              740                    745                    750
Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser
          755                    760                    765
Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu
          770                    775                    780
His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu
785                    790                    795                    800
Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala
              805                    810                    815
Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His Glu
          820                    825                    830
Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys
          835                    840                    845
Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu
          850                    855                    860
Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr
865                    870                    875                    880
Ser Asn Lys Leu Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile
              885                    890                    895
Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu
          900                    905                    910
Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val
          915                    920                    925
Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro
          930                    935                    940
Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg
945                    950                    955                    960
Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn
              965                    970                    975
Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr
          980                    985                    990
Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro
          995                    1000                   1005
Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln
      1010                   1015                   1020
Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His
1025                   1030                   1035                   1040
Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu
                  1045                   1050                   1055
Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu
          1060                   1065                   1070
Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala
          1075                   1080                   1085
Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn
      1090                   1095                   1100
Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala
1105                   1110                   1115                   1120
Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro
                  1125                   1130                   1135
Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys
              1140                   1145                   1150
Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser
          1155                   1160                   1165
Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu
      1170                   1175                   1180
Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys
1185                   1190                   1195                   1200
Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser
                  1205                   1210                   1215
Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu
      1220                   1225                   1230
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Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe
        1235                    1240                    1245
Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr
        1250                    1255                    1260
Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr
1265                    1270                    1275                    1280
Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys
                1285                    1290                    1295
Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala
                1300                    1305                    1310
Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His
            1315                    1320                    1325
Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu
        1330                    1335                    1340
Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser
1345                    1350                    1355                    1360
Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His
                1365                    1370                    1375
Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln
                1380                    1385                    1390
Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg
            1395                    1400                    1405
Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp
        1410                    1415                    1420
Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys
1425                    1430                    1435                    1440
Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met
                1445                    1450                    1455
Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His
            1460                    1465                    1470
Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly
        1475                    1480                    1485
Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys
        1490                    1495                    1500
Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val
1505                    1510                    1515                    1520
Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
                1525                    1530                    1535
Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
            1540                    1545                    1550
Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp
        1555                    1560                    1565
Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu
        1570                    1575                    1580
Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu
1585                    1590                    1595                    1600
Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile
            1605                    1610                    1615
Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met
            1620                    1625                    1630
Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln
        1635                    1640                    1645
Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp
    1650                    1655                    1660
Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe
1665                    1670                    1675                    1680
Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr
            1685                    1690                    1695
Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys
        1700                    1705                    1710
Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn
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123

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          1715              1720              1725
Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val
   1730              1735              1740
Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe
1745              1750              1755              1760
Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr
              1765              1770              1775
Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg
           1780              1785              1790
Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile
           1795              1800              1805
Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala
      1810              1815              1820
Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser
1825              1830              1835              1840
Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser
              1845              1850              1855
Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe
           1860              1865              1870
Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu
      1875              1880              1885
Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu
   1890              1895              1900
Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu
1905              1910              1915              1920
Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile
              1925              1930              1935
Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro
           1940              1945              1950
Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr
      1955              1960              1965
Met Val His Gly Met Thr Ser Ser Ser Ser Val Val
   1970              1975              1980
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O26 cont.

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129

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130

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131

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            35   40   45

Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
        50   55   60

Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
65   70   75   80

Ile Asp Glu Asp Cys Glu Lys Asp Glu Asp Ser Ser Ser Leu Cys Ser
                85   90   95

Gln Lys Gly Gly Val Ile Lys Gln Gly Trp Leu His Lys Ala Asn Val
            100   105   110

Asn Ser Thr Ile Thr Val Thr Met Lys Val Phe Lys Arg Arg Tyr Phe
            115   120   125

Tyr Leu Thr Gln Leu Pro Asp Gly Ser Tyr Ile Leu Asn Ser Tyr Lys
            130   135   140

Asp Glu Lys Asn Ser Lys Glu Ser Lys Gly Cys Ile Tyr Leu Asp Ala
145   150   155   160

Cys Ile Asp Val Val Gln Cys Pro Lys Met Arg Arg His Ala Phe Glu
                165   170   175

Leu Lys Met Leu Asp Lys Tyr Ser His Tyr Leu Ala Ala Glu Thr Glu
            180   185   190

Gln Glu Met Glu Glu Trp Leu Ile Thr Leu Lys Lys Ile Ile Gln Ile
            195   200   205

Asn Thr Asp Ser Leu Val Gln Glu Lys Lys Glu Thr Val Glu Thr Ala
            210   215   220

Gln Asp Asp Glu Thr Ser Ser Gln Gly Lys Ala Glu Asn Ile Met Ala
225   230   235   240

Ser Leu Glu Arg Ser Met His Pro Glu Leu Met Lys Tyr Gly Arg Glu
                245   250   255

Thr Glu Gln Leu Asn Lys Leu Ser Arg Gly Asp Gly Arg Gln Asn Leu
            260   265   270

140

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Asn Cys His Asp Leu Thr Phe Asn Ile Leu Gly Gln Ile Gly Asp Asn
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Ala Lys Gly Pro Pro Thr Asn Val Glu Pro Phe Phe Ile Asn Leu Ala
            325             330             335

Leu Phe Asp Val Lys Asn Asn Cys Lys Ile Ser Ala Asp Phe His Val
            340             345             350

Asp Leu Asn Pro Pro Ser Val Arg Glu Met Leu Trp Gly Ser Ser Thr
            355             360             365

Gln Leu Ala Ser Asp Gly Ser Pro Lys Gly Ser Ser Pro Glu Ser Tyr
    370             375             380

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385             390             395             400

Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile
            405             410             415

Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile
            420             425             430

Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala
        435             440             445

Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp
    450             455             460

Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp
465             470             475             480

Gly Arg Phe Ser Pro Leu Tyr Lys Gln Asp Ser Ser Lys Leu Ser Ser
            485             490             495

Glu Asp Ile Leu Lys Leu Leu Ser Glu Tyr Lys Lys Pro Glu Lys Thr
            500             505             510

Lys Leu Gln Ile Ile Pro Gly Gln Leu Asn Ile Thr Val Glu Cys Val
        515             520             525

Pro Val Asp Leu Ser Asn Cys Ile Thr Ser Ser Tyr Val Pro Leu Lys
    530             535             540

Pro Phe Glu Lys Asn Cys Gln Asn Ile Thr Val Glu Val Glu Glu Phe
545             550             555             560

Val Pro Glu Met Thr Lys Tyr Cys Tyr Pro Phe Thr Ile Tyr Lys Asn
                565             570             575

His Leu Tyr Val Tyr Pro Leu Gln Leu Lys Tyr Asp Ser Gln Lys Thr
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Phe Ala Lys Ala Arg Asn Ile Ala Val Cys Val Glu Phe Arg Asp Ser
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Asp Glu Ser Asp Ala Ser Ala Leu Lys Cys Ile Tyr Gly Lys Pro Ala
    610   615   620

Gly Ser Val Phe Thr Thr Asn Ala Tyr Ala Val Val Ser His His Asn
625   630   635   640

Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile Glu Leu Pro Ile His
            645   650   655

Leu His Gln Lys His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys
        660   665   670

Glu Ile Asn Thr Lys Gly Thr Thr Lys Lys Gln Asp Thr Val Glu Thr
        675   680   685

Pro Val Gly Phe Ala Trp Val Pro Leu Leu Lys Asp Gly Arg Ile Ile
    690   695   700

Thr Phe Glu Gln Gln Leu Pro Val Ser Ala Asn Leu Pro Pro Gly Tyr
705   710   715   720

Leu Asn Leu Asn Asp Ala Glu Ser Arg Arg Gln Cys Asn Val Asp Ile
            725   730   735

Lys Trp Val Asp Gly Ala Lys Pro Leu Leu Lys Phe Lys Ser His Leu
            740   745   750

Glu Ser Thr Ile Tyr Thr Gln Asp Leu His Val His Lys Phe Phe His
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His Cys Gln Leu Ile Gln Ser Gly Ser Lys Glu Val Pro Gly Glu Leu
    770   775   780

Ile Lys Tyr Leu Lys Cys Leu His Ala Met Glu Ile Gln Val Met Ile
785   790   795   800

Gln Phe Leu Pro Val Ile Leu Met Gln Leu Phe Arg Val Leu Thr Asn
            805   810   815

Met Thr His Glu Asp Asp Val Pro Ile Asn Cys Thr Met Val Leu Leu
        820   825   830

His Ile Val Ser Lys Cys His Glu Glu Gly Leu Asp Ser Tyr Leu Arg
        835   840   845

Ser Phe Ile Lys Tyr Ser Phe Arg Pro Glu Lys Pro Ser Ala Pro Gln
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Ala Gln Leu Ile His Glu Thr Leu Ala Thr Thr Met Ile Ala Ile Leu
865   870   875   880

Lys Gln Ser Ala Asp Phe Leu Ser Ile Asn Lys Leu Leu Lys Tyr Ser
            885   890   895

Trp Phe Phe Phe Glu Ile Ile Ala Lys Ser Met Ala Thr Tyr Leu Leu
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Glu Glu Asn Lys Ile Lys Leu Pro Arg Gly Gln Arg Phe Pro Glu Thr
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Tyr His His Val Leu His Ser Leu Leu Leu Ala Ile Ile Pro His Val
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Phe Ile Phe Asn Leu Ile Asn Asp Tyr Ile Ser Gly Phe Ser Pro Lys
            980             985             990

Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe Glu Phe Leu Gln Thr Ile
        995             1000            1005

Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met Ala Phe Ala
    1010            1015            1020

Lys Pro Lys Leu Gln Arg Val Gln Asp Ser Asn Leu Glu Tyr Ser Leu
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Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg
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Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr Glu Ile Arg Tyr Thr Ala
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Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg
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Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro
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Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu
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Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr
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Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys
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Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe
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Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr Arg Gln Ser Ser Thr Arg
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Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp Gln Tyr Glu Ile Arg Ser
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Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys Met Ile Ser Glu Asp Thr
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Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile
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Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly
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Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe
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Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe
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Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu
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Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp
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Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu
           85   90   95

Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg
           100   105   110

His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala
           115   120   125

Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn
   130   135   140

Leu Leu Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu
145   150   155   160

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Ala Arg Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser
            165   170   175

Val Asp Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro
            180   185   190

Lys Glu His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys
            195   200   205

Phe Glu Ile Glu Ile Glu Pro Leu Phe Ala Ser Ile Ala Leu Tyr Asp
    210   215   220

Val Lys Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn
225   230   235   240

Ser Asp Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala
            245   250   255

Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser
            260   265   270

Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly
            275   280   285

Asp Ile Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp
    290   295   300

Gly Gly Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu
305   310   315   320

Ser Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala
            325   330   335

Pro Ile Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu
            340   345   350

Val Thr Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg
            355   360   365

Arg Thr Leu Ala Gln Ser Arg Arg Leu Ser Glu Arg Ala Leu Ser Leu
    370   375   380

Glu Glu Asn Gly Val Gly Ser Asn Phe Lys Thr Ser Thr Leu Ser Val
385   390   395   400

Ser Ser Phe Phe Lys Gln Glu Gly Asp Arg Leu Ser Asp Glu Asp Leu
            405   410   415

Phe Lys Phe Leu Ala Asp Tyr Lys Arg Ser Ser Ser Leu Gln Arg Arg
            420   425   430

Val Lys Ser Ile Pro Gly Leu Leu Arg Leu Glu Ile Ser Thr Ala Pro
            435   440   445

Glu Ile Ile Asn Cys Cys Leu Thr Pro Glu Met Leu Pro Val Lys Pro
    450   455   460

Phe Pro Glu Asn Arg Thr Arg Pro His Lys Glu Ile Leu Glu Phe Pro
465   470   475   480

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Thr Arg Glu Val Tyr Val Pro His Thr Val Tyr Arg Asn Leu Leu Tyr
            485         490                     495

Val Tyr Pro Gln Arg Leu Asn Phe Val Asn Lys Leu Ala Ser Ala Arg
            500             505                 510

Asn Ile Thr Ile Lys Ile Gln Phe Met Cys Gly Glu Asp Ala Ser Asn
        515             520                 525

Ala Met Pro Val Ile Phe Gly Lys Ser Ser Gly Pro Glu Phe Leu Gln
        530             535             540

Glu Val Tyr Thr Ala Val Thr Tyr His Asn Lys Ser Pro Asp Phe Tyr
545                 550                 555                 560

Glu Glu Val Lys Ile Lys Leu Pro Ala Lys Leu Thr Val Asn His His
            565                 570                 575

Leu Leu Phe Thr Phe Tyr His Ile Ser Cys Gln Gln Lys Gln Gly Ala
        580             585                 590

Ser Val Glu Thr Leu Leu Gly Tyr Ser Trp Leu Pro Ile Leu Leu Asn
        595             600             605

Glu Arg Leu Gln Thr Gly Ser Tyr Cys Leu Pro Val Ala Leu Glu Lys
    610             615                 620

Leu Pro Pro Asn Tyr Ser Met His Ser Ala Glu Lys Val Pro Leu Gln
625             630                 635                 640

Asn Pro Pro Ile Lys Trp Ala Glu Gly His Lys Gly Val Phe Asn Ile
            645                 650                 655

Glu Val Gln Ala Val Ser Ser Val His Thr Gln Asp Asn His Leu Glu
        660             665                 670

Lys Phe Phe Thr Leu Cys His Ser Leu Glu Ser Gln Val Thr Phe Pro
        675             680                 685

Ile Arg Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu
    690             695                 700

Leu Lys Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu
705             710                 715                 720

Val Leu Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val
            725                 730                 735

Gln Pro Met Val Ile Ala Gly Gln Thr Ala Asn Phe Ser Gln Phe Ala
            740             745                 750

Phe Glu Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp
        755             760                 765

Leu Ser Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val
        770             775                 780

His Tyr Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser
785                 790                 795                 800

Gly Ala Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly
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Arg Thr Ser Ala Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val
    820   825   830

Met Ser Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp
    835   840   845

Glu Glu Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys
 850   855   860

Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser
865   870   875   880

Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu
      885   890   895

Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln
    900   905   910

His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe
    915   920   925

Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr
    930   935   940

Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln
945   950   955   960

Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu
    965   970   975

Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys
    980   985   990

Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met
    995   1000   1005

Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn
   1010   1015   1020

Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys
1025   1030   1035   1040

Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp
      1045   1050   1055

Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln
    1060   1065   1070

His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp
    1075   1080   1085

Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala
   1090   1095   1100

Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys
1105   1110   1115   1120

Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly
    1125   1130   1135

Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp
        1140   1145   1150

Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala
        1155   1160   1165

Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe
    1170   1175   1180

Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln
1185   1190   1195   1200

Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe
        1205   1210   1215

Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile
        1220   1225   1230

Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe
        1235   1240   1245

Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys
    1250   1255   1260

Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu
1265   1270   1275   1280

Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg
        1285   1290   1295

Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu
        1300   1305   1310

Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu
    1315   1320   1325

Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn
    1330   1335   1340

Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile
1345   1350   1355   1360

Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly
        1365   1370   1375

Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr
        1380   1385   1390

Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe
    1395   1400   1405

Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys
    1410   1415   1420

His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser
1425   1430   1435   1440

Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala
        1445   1450   1455

150

Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala
        1460   1465   1470

Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg
      1475   1480   1485

Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln
    1490   1495   1500

Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn
1505   1510   1515   1520

Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro
            1525   1530   1535

Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala
        1540   1545   1550

Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His
      1555   1560   1565

Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala
    1570   1575   1580

Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr
1585   1590   1595   1600

Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu
            1605   1610   1615

Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly
        1620   1625   1630

Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu
        1635   1640   1645

Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val
    1650   1655   1660

Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu
1665   1670   1675   1680

Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp
            1685   1690   1695

Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg
        1700   1705   1710

Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe
        1715   1720   1725

Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg
    1730   1735   1740

Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val
1745   1750   1755   1760

Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys
            1765   1770   1775

Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu

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Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg
      1795   1800   1805

Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu
  1810   1815   1820

Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala
1825   1830   1835   1840

Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe
     1845   1850   1855

Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr
    1860   1865   1870

Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met
    1875   1880   1885

Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly
    1890   1895   1900

Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro
1905   1910   1915   1920

Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe
      1925   1930   1935

Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr
     1940   1945   1950

Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys
      1955   1960   1965

Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu
    1970   1975   1980

Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His
1985   1990   1995   2000

Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser
      2005   2010   2015

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<212> PRT
<213> Homo sapiens

<220>
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Ala Glu Val Arg Lys Gln Ile Ser Gly Gln Tyr Ser Gly Ser Pro Gln
       20   25   30

Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr

Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu
    50   55   60

Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile
65   70   75   80

Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys
            85   90   95

Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His
            100   105   110

Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile
        115   120   125

Arg Lys Tyr His Lys Leu Gly Thr Gly Phe Asn Pro Asn Thr Leu Asp
    130   135   140

Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro Lys Gln Val Phe Glu Ser
145   150   155   160

Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu
            165   170   175

Lys Arg Arg Ser Met Ser Ile Asp Asp Thr Pro Arg Gly Ser Trp Ala
            180   185   190

Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu Pro Asp Ala Leu Leu Pro
        195   200   205

Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu Ile Asp Arg Gln Asn Asp
    210   215   220

Asp Gln Arg Lys Ser Asn Arg His Lys Glu Leu Phe Ala Leu His Pro
225   230   235   240

Ser Pro Asp Glu Glu Glu Pro Ile Glu Arg Leu Ser Val Pro Asp Ile
            245   250   255

Pro Lys Glu His Phe Gly Gln Arg Leu Leu Val Lys Cys Leu Ser Leu
            260   265   270

Lys Phe Glu Ile Glu Ile Glu Pro Ile Phe Ala Ser Leu Ala Leu Tyr
        275   280   285

Asp Val Lys Glu Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu
    290   295   300

Asn Ser Glu Gln Met Lys Gly Leu Leu Arg Pro His Val Pro Pro Ala
305   310   315   320

Ala Ile Thr Thr Leu Ala Arg Ser Ala Ile Phe Ser Ile Thr Tyr Pro
            325   330   335

Ser Gln Asp Val Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln
            340   345   350

Gly Asp Ile Gly Glu Cys Ala Glu Pro Tyr Met Ile Phe Lys Glu Ala
    355   360   365

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Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala
    370             375             380

Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp
385             390·            395                     400

Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu
            405             410                 415

Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser
        420             425             430

Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu
        435             440             445

Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro
    450             455             460

Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu
465             470             475                     480

Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser
            485             490             495

Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp
        500             505             510

Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu
        515             520             525

Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu
    530             535             540

Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr
545             550             555                     560

Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg
            565             570             575

Gln Gly Ser Ala Arg Asn Ile Thr Val Lys Val Gln Phe Met Tyr Gly
        580             585             590

Glu Asp Pro Ser Asn Ala Met Pro Val Ile Phe Gly Lys Ser Ser Cys
    595             600             605

Ser Glu Phe Ser Lys Glu Ala Tyr Thr Ala Val Val Tyr His Asn Arg
    610             615             620

Ser Pro Asp Phe His Glu Glu Ile Lys Val Lys Leu Pro Ala Thr Leu
625             630             635                     640

Thr Asp His His His Leu Leu Phe Thr Phe Tyr His Val Ser Cys Gln
            645             650             655

Gln Lys Gln Asn Thr Pro Leu Glu Thr Pro Val Gly Tyr Thr Trp Ile
        660             665             670

Pro Met Leu Gln Asn Gly Arg Leu Lys Thr Gly Gln Phe Cys Leu Pro
    67,5            680             685
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154

Val Ser Leu Glu Lys Pro Pro Gln Ala Tyr Ser Val Leu Ser Pro Glu
    690   695   700

Val Pro Leu Pro Gly Met Lys Trp Val Asp Asn His Lys Gly Val Phe
705   710   715   720

Asn Val Glu Val Val Ala Val Ser Ser Ile His Thr Gln Asp Pro Tyr
                725   730   735

Leu Asp Lys Phe Phe Ala Leu Val Asn Ala Leu Asp Glu His Leu Phe
            740   745   750

Pro Val Arg Ile Gly Asp Met Arg Ile Met Glu Asn Asn Leu Glu Asn
            755   760   765

Glu Leu Lys Ser Ser Ile Ser Ala Leu Asn Ser Ser Gln Leu Glu Pro
    770   775   780

Val Val Arg Phe Leu His Leu Leu Leu Asp Lys Leu Ile Leu Leu Val
785   790   795   800

Ile Arg Pro Pro Val Ile Ala Gly Gln Ile Val Asn Leu Gly Gln Ala
            805   810   815

Ser Phe Glu Ala Met Ala Ser Ile Ile Asn Arg Leu His Lys Asn Leu
            820   825   830

Glu Gly Asn His Asp Gln His Gly Arg Asn Ser Leu Leu Ala Ser Tyr
            835   840   845

Ile His Tyr Val Phe Arg Leu Pro Asn Thr Tyr Pro Asn Ser Ser Ser
    850   855   860

Pro Gly Pro Gly Gly Leu Gly Gly Ser Val His Tyr Ala Thr Met Ala
865   870   875   880

Arg Ser Ala Val Arg Pro Ala Ser Leu Asn Leu Asn Arg Ser Arg Ser
            885   890   895

Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp
    900   905   910

Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn
    915   920   925

Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn
    930   935   940

Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn
945   950   955   960

Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr
            965   970   975

Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln
            980   985   990

Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala
    995   1000   1005

Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr

155

Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg
1025　　　　　　　　　1030　　　　　　　　　1035　　　　　　　　　1040

Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile
　　　　　　　　　1045　　　　　　　　　1050　　　　　　　　　1055

Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr
　　　　　　1060　　　　　　　　　1065　　　　　　　　　1070

Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly
　　　　　1075　　　　　　　　　1080　　　　　　　　　1085

Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys
　　　1090　　　　　　　　　1095　　　　　　　　　1100

Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp
1105　　　　　　　　　1110　　　　　　　　　1115　　　　　　　　　1120

Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu
　　　　　　　　1125　　　　　　　　　1130　　　　　　　　　1135

Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser
　　　　　1140　　　　　　　　　1145　　　　　　　　　1150

Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln
　　　　1155　　　　　　　　　1160　　　　　　　　　1165

Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His
　　　1170　　　　　　　　　1175　　　　　　　　　1180

Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro
1185　　　　　　　　1190　　　　　　　　　1195　　　　　　　　　1200

Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val
　　　　　　　1205　　　　　　　　　1210　　　　　　　　　1215

His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro
　　　　　　1220　　　　　　　　　1225　　　　　　　　　1230

Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile
　　　　1235　　　　　　　　　1240　　　　　　　　　1245

Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn
　　　1250　　　　　　　　　1255　　　　　　　　　1260

Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu
1265　　　　　　　　　1270　　　　　　　　　1275　　　　　　　　　1280

Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr
　　　　　　　1285　　　　　　　　　1290　　　　　　　　　1295

Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr
　　　　　　1300　　　　　　　　　1305　　　　　　　　　1310

Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu
　　　　1315　　　　　　　　　1320　　　　　　　　　1325

Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu
　　　1330　　　　　　　　　1335　　　　　　　　　1340

Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu
1345   1350   1355   1360

Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys
          1365   1370   1375

Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met
          1380   1385   1390

Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln
          1395   1400   1405

Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly
          1410   1415   1420

Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr
1425   1430   1435   1440

His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile
          1445   1450   1455

Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu
          1460   1465   1470

Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr
          1475   1480   1485

Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His
          1490   1495   1500

Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala
1505   1510   1515   1520

Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu
          1525   1530   1535

Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys
          1540   1545   1550

Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr
          1555   1560   1565

Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val
          1570   1575   1580

Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln
1585   1590   1595   1600

Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr
          1605   1610   1615

Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln
          1620   1625   1630

Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val
          1635   1640   1645

Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met
          1650   1655   1660

Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp
1665   1670   1675   1680

Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu
            1685   1690   1695

Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu
            1700   1705   1710

Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe
        1715   1720   1725

Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp
        1730   1735   1740

Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr
1745   1750   1755   1760

Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser
            1765   1770   1775

Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile
            1780   1785   1790

Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His
        1795   1800   1805

Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly
        1810   1815   1820

Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr
1825   1830   1835   1840

Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala
            1845   1850   1855

Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly
        1860   1865   1870

Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro
        1875   1880   1885

Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr
    1890   1895   1900

Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr
1905   1910   1915   1920

Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro
            1925   1930   1935

Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys
        1940   1945   1950

Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr
        1955   1960   1965

Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu
    1970   1975   1980

Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala

158

Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln
                    2005   2010   2015

Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln
               2020   2025   2030

Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His
          2035   2040   2045

Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp
     2050   2055   2060

Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr
2065   2070   2075   2080

Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro
               2085   2090

<210> 138
<211> 2047
<212> PRT
<213> Homo sapiens

<220>
<223> CLASP-7 amino acid sequence

<400> 138
Met Ala Ala Ser Glu Arg Arg Ala Phe Ala His Lys Ile Asn Arg Thr
1   5   10   15

Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg Ser Gly Ser
               20   25   30

Pro His Ser Ser Arg Arg Cys Ser Ser Leu Gly Val Pro Leu Thr
          35   40   45

Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
     50   55   60

Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
65   70   75   80

Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
               85   90   95

Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala
               100   105   110

Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln
          115   120   125

Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu
     130   135   140

Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly
145   150   155   160

Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser

159

Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe
        180   185   190

Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu
        195   200   205

Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg
    210   215   220

Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu
225   230   235   240

Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His
            245   250   255

Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile
            260   265   270

Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu
        275   280   285

Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser
    290   295   300

Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr
305   310   315   320

Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile
            325   330   335

Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser
            340   345   350

Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys
        355   360   365

Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys
    370   375   380

Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His
385   390   395   400

Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp
            405   410   415

Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly
        420   425   430

Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly
        435   440   445

Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala
    450   455   460

Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg
465   470   475   480

Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu
            485   490   495

Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser
        500   505   510

Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro
        515   520   525

Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His
    530   535   540

Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe
545   550   555   560

Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr
            565   570   575

Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys
            580   585   590

Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr
        595   600   605

His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro
    610   615   620

Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val
625   630   635   640

Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe
            645   650   655

Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe
            660   665   670

Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu
        675   680   685

Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys
    690   695   700

Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln
705   710   715   720

Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu
            725   730   735

Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn
            740   745   750

Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser
            755   760   765

Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val
        770   775   780

Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu
785   790   795   800

Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His
            805   810   815

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Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu
        820   825   830

Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser
        835   840   845

Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala
    850   855   860

Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser
865   870   875   880

Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp
                885   890   895

Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu
            900   905   910

Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu
        915   920   925

Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu
    930   935   940

His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe
945   950   955   960

Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly
                965   970   975

Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His
            980   985   990

Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val
        995   1000   1005

Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val
    1010   1015   1020

Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu
1025   1030   1035   1040

Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr
            1045   1050   1055

Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro
            1060   1065   1070

Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala
        1075   1080   1085

Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg
    1090   1095   1100

Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala
1105   1110   1115   1120

Leu Glu Pro Glu Ala Glu Gly Ala Phe Leu Leu His Lys Lys Ala Ile
            1125   1130   1135

Ser Ala Val His Ser Leu Leu Cys Gly His Asp Thr Asp Pro Arg Tyr

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Ala Glu Ala Thr Val Lys Ala Arg Val Ala Glu Leu Tyr Leu Pro Leu
      1155   1160   1165

Leu Ser Ile Ala Arg Asp Thr Leu Pro Arg Leu His Asp Phe Ala Glu
    1170   1175   1180

Gly Pro Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr
1185   1190   1195   1200

Glu Gly Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met
          1205   1210   1215

Ala Ile Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser
        1220   1225   1230

Gln Gly Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu
      1235   1240   1245

Ser Ser Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr
    1250   1255   1260

Glu Pro Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln
1265   1270   1275   1280

Leu Gly Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu
          1285   1290   1295

Tyr Lys Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys
          1300   1305   1310

Lys Ser Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr
    1315   1320   1325

Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro
    1330   1335   1340

Phe Gly Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp
1345   1350   1355   1360

Lys Gln Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His
          1365   1370   1375

Glu Ala Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val
        1380   1385   1390

Leu Asp Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala
        1395   1400   1405

Arg Glu Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu
    1410   1415   1420

Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln
1425   1430   1435   1440

Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr
        1445   1450   1455

Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser
        1460   1465   1470

Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu
       1475   1480   1485

Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met
       1490   1495   1500

Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe
1505   1510   1515   1520

Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala
              1525   1530   1535

Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln
         1540   1545   1550

Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met
         1555   1560   1565

Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg
    1570   1575   1580

Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu
1585   1590   1595   1600

Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala
              1605   1610   1615

Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala
         1620   1625   1630

Leu Leu Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln
         1635   1640   1645

Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile
    1650   1655   1660

Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu
1665   1670   1675   1680

Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met
              1685   1690   1695

Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro
         1700   1705   1710

Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly
         1715   1720   1725

Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp
    1730   1735   1740

Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His
1745   1750   1755   1760

Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile
              1765   1770   1775

Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu
         1780   1785   1790

Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val
        1795   1800   1805

Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr
        1810   1815   1820

Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr
1825   1830   1835   1840

Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe
        1845   1850   1855

Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg
        1860   1865   1870

Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg
        1875   1880   1885

Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val
        1890   1895   1900

Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr
1905   1910   1915   1920

Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly
        1925   1930   1935

Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val
        1940   1945   1950

Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn
        1955   1960   1965

Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala
        1970   1975   1980

Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His
1985   1990   1995   2000

Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro
        2005   2010   2015

Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly
        2020   2025   2030

Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu
        2035   2040   2045

<210> 139
<211> 2180
<212> PRT
<213> Homo sapiens

<220>
<223> CLASP-1 amino acid sequence

<400> 139
Met Ser Phe Arg Gly Lys Val Phe Lys Arg Glu Pro Ser Glu Phe Trp
    1   5   10   15

Lys Lys Arg Arg Thr Val Arg Arg Val Ile Gln Glu Glu Phe His Arg
            20   25   30

Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu
        35   40   45

Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln
    50   55   60

Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser
65   70   75   80

Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His
            85   90   95

Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser
            100   105   110

Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile
        115   120   125

Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His
    130   135   140

Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr
145   150   155   160

Ser His Ser Ser Ser Lys Gly Gly Gly Gly Ala Gly Gly Thr Gly Val
            165   170   175

Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn
        180   185   190

Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr
        195   200   205

Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys
    210   215   220

Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly
225   230   235   240

Val Val Gln Asn Asn Arg Leu Arg Lys Tyr Ala Phe Glu Leu Lys Met
            245   250   255

Asn Asp Leu Thr Tyr Phe Val Leu Ala Ala Glu Thr Glu Ser Asp Met
        260   265   270

Asp Glu Trp Ile His Thr Leu Asn Arg Ile Leu Gln Ile Ser Pro Glu
        275   280   285

Gly Pro Leu Gln Gly Arg Arg Ser Thr Glu Leu Thr Asp Leu Gly Leu
    290   295   300

Asp Ser Leu Asp Asn Ser Val Thr Cys Glu Cys Thr Pro Glu Glu Thr
305   310   315   320

Asp Ser Ser Glu Asn Asn Leu His Ala Asp Phe Ala Lys Tyr Leu Thr
            325   330   335

Glu Thr Glu Asp Thr Val Lys Thr Thr Arg Asn Met Glu Arg Leu Asn

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            340                        345                        350

Leu Phe Ser Leu Asp Pro Asp Ile Asp Thr Leu Lys Leu Gln Lys Lys
        355                 360                 365

Asp Leu Leu Glu Pro Glu Ser Val Ile Lys Pro Phe Glu Glu Lys Ala
    370                 375                 380

Ala Lys Arg Ile Met Ile Ile Cys Lys Ala Leu Asn Ser Asn Leu Gln
385                 390                 395                 400

Gly Cys Val Thr Glu Asn Glu Asn Asp Pro Ile Thr Asn Ile Glu Pro
                405                 410                 415

Phe Phe Val Ser Val Ala Leu Tyr Asp Leu Arg Asp Ser Arg Lys Ile
            420                 425                 430

Ser Ala Asp Phe His Val Asp Leu Asn His Ala Ala Val Arg Gln Met
        435                 440                 445

Leu Leu Gly Ala Ser Val Ala Leu Glu Asn Gly Asn Ile Asp Thr Ile
    450                 455                 460

Thr Pro Arg Gln Ser Glu Glu Pro His Ile Lys Gly Leu Pro Glu Glu
465                 470                 475                 480

Trp Leu Lys Phe Pro Lys Gln Ala Val Phe Ser Val Ser Asn Pro His
            485                 490                 495

Ser Glu Ile Val Leu Val Ala Lys Ile Glu Lys Val Leu Met Gly Asn
            500                 505                 510

Ile Ala Ser Gly Ala Glu Pro Tyr Ile Lys Asn Pro Asp Ser Asn Lys
        515                 520                 525

Tyr Ala Gln Lys Ile Leu Lys Ser Asn Arg Gln Phe Cys Ser Lys Leu
    530                 535                 540

Gly Lys Tyr Arg Arg Ala Phe Ala Trp Ala Val Arg Ser Val Phe Lys
545                 550                 555                 560

Asp Asn Gln Gly Asn Val Asp Arg Asp Ser Arg Phe Ser Pro Leu Phe
                565                 570                 575

Arg Gln Glu Ser Ser Lys Ile Ser Thr Glu Asp Leu Val Lys Leu Val
            580                 585                 590

Ser Asp Tyr Arg Arg Ala Asp Arg Ile Ser Lys Met Gln Thr Ile Pro
        595                 600                 605

Gly Ser Leu Asp Ile Ala Val Asp Asn Val Pro Leu Glu His Pro Asn
    610                 615                 620

Cys Val Thr Ser Ser Phe Ile Pro Val Lys Pro Phe Asn Met Met Ala
625                 630                 635                 640

Gln Thr Glu Pro Thr Val Glu Val Glu Glu Phe Val Tyr Asp Ser Thr
                645                 650                 655

Lys Tyr Cys Arg Pro Tyr Arg Val Tyr Lys Asn Gln Ile Tyr Ile Tyr
        660                 665                 670


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Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg
        675             680             685

Asn Ile Thr Val Cys Ile Glu Phe Lys Asn Ser Asp Glu Glu Ser Ala
    690             695             700

Lys Pro Leu Lys Cys Ile Tyr Gly Lys Pro Glu Gly Pro Leu Phe Thr
705             710             715                     720

Ser Ala Ala Tyr Thr Ala Val Leu His His Ser Gln Asn Pro Asp Phe
            725             730             735

Ser Asp Glu Val Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His
            740             745             750

His Ile Leu Phe Ser Phe Tyr His Val Thr Cys Asp Ile Asn Ala Lys
        755             760             765

Ala Asn Ala Lys Lys Lys Glu Ala Leu Glu Thr Ser Val Gly Tyr Ala
    770             775             780

Trp Leu Pro Leu Met Lys His Asp Gln Ile Ala Ser Gln Glu Tyr Asn
785             790             795                     800

Ile Pro Ile Ala Thr Ser Leu Pro Pro Asn Tyr Leu Ser Phe Gln Asp
            805             810             815

Ser Ala Ser Gly Lys His Gly Gly Ser Asp Ile Lys Trp Val Asp Gly
            820             825             830

Gly Lys Pro Leu Phe Lys Val Ser Thr Phe Val Val Ser Thr Val Asn
        835             840             845

Thr Gln Asp Pro His Val Asn Ala Phe Phe Gln Glu Cys Gln Lys Arg
    850             855             860

Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys
865             870             875                     880

Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu
            885             890             895

Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu
            900             905             910

Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala
        915             920             925

Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys
    930             935             940

Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp
945             950             955                     960

Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr
            965             970             975

Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu
            980             985             990
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Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro
        995   1000   1005

Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu
    1010   1015   1020

Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr Lys Asp Ala Leu
1025   1030   1035   1040

Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg Phe Leu Lys Arg
            1045   1050   1055

Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn
            1060   1065   1070

Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr
        1075   1080   1085

Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro
    1090   1095   1100

Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro
1105   1110   1115   1120

Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser
            1125   1130   1135

Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu
            1140   1145   1150

Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu
        1155   1160   1165

Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp
    1170   1175   1180

Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met
1185   1190   1195   1200

Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys
            1205   1210   1215

Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp
        1220   1225   1230

Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His
        1235   1240   1245

Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile
    1250   1255   1260

Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser
1265   1270   1275   1280

Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys
            1285   1290   1295

Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala
            1300   1305   1310

Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr

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          1315                1320                1325
Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr
     1330                1335                1340
Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser
1345                1350                1355                1360
Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn Phe Arg Tyr Leu
               1365                1370                1375
Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val
          1380                1385                1390
Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys
          1395                1400                1405
Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His
     1410                1415                1420
Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly
1425                1430                1435                1440
Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr
               1445                1450                1455
Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr
          1460                1465                1470
Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val
          1475                1480                1485
Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys
          1490                1495                1500
Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe
1505                1510                1515                1520
Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu
               1525                1530                1535
Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala
          1540                1545                1550
Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His
          1555                1560                1565
Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe
     1570                1575                1580
Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser
1585                1590                1595                1600
His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly
               1605                1610                1615
Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe
          1620                1625                1630
Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val
          1635                1640                1645


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Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln
    1650   1655   1660

Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr
1665   1670   1675   1680

Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp
         1685   1690   1695

Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu
         1700   1705   1710

Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu
         1715   1720   1725

Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu
    1730   1735   1740

Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr
1745   1750   1755   1760

Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser
         1765   1770   1775

Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly
         1780   1785   1790

Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr
         1795   1800   1805

Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala
    1810   1815   1820

Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe
1825   1830   1835   1840

Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys
         1845   1850   1855

Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr
         1860   1865   1870

Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys
         1875   1880   1885

Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser
    1890   1895   1900

Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val
1905   1910   1915   1920

Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro
         1925   1930   1935

Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu
         1940   1945   1950

Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile
    1955   1960   1965

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Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His
    1970   1975   1980

Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser
1985   1990   1995   2000

His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser
         2005   2010   2015

Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg
         2020   2025   2030

Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met
         2035   2040   2045

Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn
    2050   2055   2060

Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala
2065   2070   2075   2080

Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg
         2085   2090   2095

Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu
         2100   2105   2110

Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr
         2115   2120   2125

Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr
    2130   2135   2140

Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg
2145   2150   2155   2160

Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val Ser Ile Ser Ser
         2165   2170   2175

Ser Ala Glu Val
         2180

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<400> 140
aggccttgtc tctgtttacc tg   22

<210> 141
<211> 23
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<400> 141
acaggaacct gctgtacgtg tac   23

172

<210> 142
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<212> DNA
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<400> 142
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<210> 149
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